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(54) Title: GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG KNOWN GENES AND PROTEINS

(57) Abstract

The present invention relates to methods for identifying novel genes comprising: (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest. The present invention also relates to natural language processing and extraction of relational information associated with genes and proteins that are found in genomics journal articles. To enable access to information in textual form, the natural language processing system of the present invention provides a method for extracting and structuring information found in the literature in a form appropriate for subsequent applications.

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GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG KNOWN GENES AND PROTEINS

SPECIFICATION

The invention described herein was funded in part by a grant from the National Library of Medicine, namely, Grant Number's LM06274 and LM05627. The United States Government may have certain rights to the invention. The present specification contains a computer program listing which appears as a microfiche Appendix H.

STATEMENT REGARDING MATERIAL SUBJECT TO COPYRIGHT

An appendix containing source code listing utilized in practicing an exemplary embodiment of the invention is included as part of the Specification.

1. INTRODUCTION

The present invention relates to methods for identifying novel genes comprising: (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The present invention relates to natural language processing and extraction of relational information associated with genes and proteins that are found

in genomics journal articles. To enable access to information in textual form, the natural language processing system of the present invention provides a method for extracting and structuring information found in the literature in a form appropriate for subsequent applications. Specifically, the present invention provides for the generation of specialized databases containing information on gene/protein structure, function and regulatory interactions based on the retrieval of such information from research articles and databases, and computer representation of such information in a manner that allows efficient access to the extracted information.

The invention further provides for the use of the specialized databases for identifying novel genes based on detection of sequence similarities and domain/motif matches between genes/proteins, computation and interpretation of phylogenetic trees for multigene families, and analysis of homologous regulatory networks. The methods of the invention are based on the observation that functionally similar regulatory systems are generated during evolution by genetic duplication of ancestral genes. Thus, a comparison of homologous/similar networks within the same organism and between different species will allow the identification of genes absent in one of the systems under comparison. In this way genes that contribute to the phenotype of a specific disease associated with a particular biological system under analysis may be identified.

2. BACKGROUND OF THE INVENTION

2.1. NATURAL LANGUAGE PROCESSING

Researchers working in molecular biology must constantly consider the information present in the literature relating to their regulatory systems of interest and the genes and proteins that operate within those systems. Unfortunately, to remain up-to-date on the relevant literature, the researcher is required to perform laborious reading and manual integration of research articles, each of which may address a narrow subject. Therefore, technology that enables rapid retrieval of information from literature and manipulation of derived functional data should have a dramatic effect on the accesss of the researcher to important facts and ultimately should facilitate the discovery of novel human genes.

Natural language processing is an automated system that provides for a complex of programs for automatic retrieval of information from text analysis and for the computer representation of that information in a form that allows efficient access and extraction of that information. MedLee (Medical Language Extraction and Encoding System) has recently been successfully used for processing different types of medical texts as described in co-pending United States Patent Application Serial Number 09/370,329, incorporated herein in its entirety by reference (see also, Friedman et al., 1994, J. Amer. Med. Inf. Assoc. 1:161-174; Hripcsak et al. 1995, Ann. Intern. Med. 122:681-688; Hripcsak et al., 1998, Meth. Inform. Med.; Jain et al., 1996, Proc. AMIA Annu. Fall Symp. 542-546; Knirsch et al., 1998). When tested, MedLEE was on average as successful in retrieving reports associated with specified clinical connections as twelve medical experts invited for evaluation of the system.

Another text analysis technique has recently been developed that combines finite-state machines with statistical machine learning approaches. These models extract detailed semantic information from texts (e.g., see Hatzivassiloglou 1996, In Klavens, J.L., and Resnick, P.S. (eds) *The Balancing Act: Combining Symbolic and Statistical Approaches to Language*, MIT Press, Cambridge, MA) when extensive prior knowledge about the domain is not available. The techniques have been subsequently applied to the tasks of (i) automatically identifying medical terms for the automated summarization of research articles reporting on clinical studies and (ii) sanitizing sensitive information in patient records so that they can be widely disseminated for research purposes.

A number of projects have also been developed as statistical information extraction tools that operate with limited or no prior knowledge about the application domain. These earlier efforts include XTRACT, a tool that recovers collocational restrictions between words that has been licensed to more than thirty sites worldwide (Smadja, F., 1993, J. Comp. Ling. 19:143-177), CHAMPOLLION, a system that retrieves bilingual mappings between words and phrases in parallel texts from different languages (Smadja, F. et al. 1996, J. Computational Linguistics 22:1-38), and a system that automatically aligns noisy, semi-parallel texts from different languages (Fung, P. and McKeown, K.R., 1997, Machine Translation 11:23-29).

2.2. IDENTIFICATION OF NOVEL GENES

A variety of different methods are currently utilized for the identification and characterization of novel genes. Perhaps the most widely used method for generating large quantities of sequence information is via high throughput nucleotide sequencing of random DNA fragments. A disadvantage associated with this gene discovery technique is that in most instances when genes are identified their function is unknown.

For identification of specific disease genes, positional cloning is currently the most widely used method. The positional cloning approach combines methods of formal genetics, physical mapping and mutation analysis and usually starts with a precise description of the disease phenotype and a tracing of the disease through families of affected individuals. Genetic linkage data obtained from the analysis of affected families frequently allows the determination of an approximate genomic localization of the candidate disease gene with a precision of several millions of nucleotides. Once localized, the genetically defined chromosomal region is then recovered from genomic libraries as a contiguous set of genomic fragments. Genes residing in the disease-related region are determined by analysis of transcripts that are transcribed from the genomic fragment. From this analysis an initial set of candidate genes for a particular disease are identified based on the presence of the gene product in the biological system affected by disease and a correlation between its expression pattern and the pattern of disease progression.

Important information for selection of candidate genes also comes from analysis of their homology with genes known to be part of the same or related biological system. Finally, the ultimate proof of association between a gene and a genetic disorder comes from mutational analysis of a gene in patients affected by the disorder and from demonstration of a statistical correlation between occurrence of mutation and the disease phenotype.

Although positional cloning is a powerful method for gene discovery, the experimental method is extremely tedious and expensive. Moreover, disease genes implicated in genetically complex disorders, *i.e.*, those controlled by multiple

loci, can hardly be found using this strategy because of the complications associated with multiple loci linkage analysis.

Specialized databases for homology searches have also been utilized in disease gene discovery projects. In recent years a number of efficient sequence comparison tools have been developed such as the BLAST (Basic Local Alignment Search Tool) family of programs designed for comparison of a single "search sequence" with a database (see Altschul et al., 1990, J. Mol. Biol. 215:403-410; Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402), the family of Hidden Markov Model methods for comparison of a set of aligned sequences that usually represent a protein motif or domain with a database (e.g., Krogh et al., 1994, J. Mol. Biol. 235:1501-1531; Grundy et al., 1997, Biochem Biophys. Res. Commun. 231:760-6) and various other comparison tools (Wu et al., 1996, Comput. Appl. Biosci 12:109-118; Neuwald et al., 1995, Protein Sci. 4:1618-1632; Neuwald, 1997, Nucleic Acids Res. 25:1665-1677).

When used in disease gene discovery projects, homology searches can be enhanced by creating specialized databases that utilize statistical analysis for evaluating significance of sequence similarities in comparison of new sequences with a database of known sequence. Such databases are fine-tuned to the size of the database used (Altschul et al., 1990, J. Mol. Biol. 215:403-410; Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402), so that the same level of homology between a search sequence and a database sequence can be determined to be highly significant if the search sequence is compared with a smaller database, or insignificant and thus undetectable, if the search sequence is compared with a larger database.

In alternatives to standard homology searches, in projects oriented towards gene discovery, researchers usually have some *a priori* knowledge about the set of genes/proteins that might display important similarity to the unknown new gene. Therefore, selecting an *a priori* defined set of genes/proteins for comparison with new experimental sequences is a feasible and useful strategy. This strategy was successfully applied to search for homologs of disease genes in yeast and nematode genomes by Mushegian et al. (1997, Proc. Natl. Acad. Sci USA 94:5831-5836).

Two homologous genes taken from different species that originate from the nearest common ancestor by speciation are referred to as orthologs, while any two genes that originate from a common ancestor via a series of events involving intragenomic duplications are call paralogs. Tatusov et al. (1994, Proc. Nat.l, Acad. Sci USA 91:12091-12095) describe comparisons of proteins encoded by the genomes of different phylogenetic lineages and elucidation of consistent patterns of sequence similarities permitting the delineation of clusters of orthologous groups (COGs). Each COG consists of individual orthologous genes or orthologous groups of paralogs from different phylogenetic lineages. Since orthologs typically have the same function, the classification of known genes and proteins into clusters of orthologous groups permits the assignment of a function to a newly discovered gene or protein by merely classifying it into a COG. Although Tatusov describes a method for assigning a function to a newly discovered gene, he does not describe a method for predicting the existence of undiscovered genes. In addition, Yuan, et al. attempted simultaneous reconstruction of a species tree and identification of paralogous groups of sequences and detection of orthologs in sequence databases (Yuan et al., 1998, *Bioinformatics* 143:285-289).

Other groups have aimed at capturing interactions among molecules through the use of programs designed to compare structures and functions of proteins (Kazic 1994, In: Molecular Modeling: From Virtual Tools to Real Problems, Kumosinski, T. and Liebman, M.N. (Eds.), American Chemical Society, Washington, D.C. pp. 486-494; Kazic, 1994, In: New Data Challenges in Our Information Age Glaesar, P.S. and Millward, M.T.L. (Eds.). Proceedings of the Thirteenth International CODATA Secretariat, Paris pp. C133-C140; Goto et al., 1997, Pac. Symp. Biocomput. p. 175-186; Bono et al., 1998, Genome Res. 8:203-210; Selkov et al., 1996, Nucleic Acids Res. 24:26-28). These projects are significantly different from the inventive methods described herein because they do not describe methods for deducing the existence of as yet unknown genes based on comparisons of regulatory pathways and gene structure between one or more species. The present invention provides a method for increasing the sensitivity of analysis methods through the generation of specialized databases.

3. SUMMARY OF THE INVENTION

In accordance with the present invention there is provided methods for identification of novel genes comprising (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The invention is based, in part, on the observation that functionally similar regulatory systems are generated during evolution by genetic duplication of ancestral genes. Thus, by comparing phylogenetic trees or regulatory networks and identifying genes and/or proteins absent in one system under comparison, the existence of as yet unidentified genes and/or proteins can be predicted. To make meaningful comparisons of phylogenetic trees it is necessary to distinguish between orthologs and paralogs. The present invention provides a method useful for discriminating between orthologs and paralogs and inferring the existence of as yet unidentified genes and/or proteins.

The present invention relates to natural language processing and extraction of relational information associated with genes and proteins that are found in genomics journal articles. Specifically, the natural language processing system of the invention is used to parse the articles published in biological journals focusing on structure and interactions among genes and proteins followed by computer representation of such interactions.

In accordance with the present invention, specialized databases are developed that contain information on gene/protein structure and interactions based on information derived from preexisting databases and/or research articles including information on interactions among genes and proteins, their domain/motif structure and their subcellular and tissue expression/distribution patterns.

The invention relates to a sequence analysis program which utilizes the specialized database for comparison of a single sequence, processing the output into a sequence alignment, computing phylogenetic trees, and analyzing these trees to

predict undiscovered genes. This program also includes a set of tools for generating motif/domain models from multiple sequence alignments of known genes and for using these models for extraction of structurally and/or functionally homologous sequences from databases which contain raw sequence data.

The invention further provides for a simulation and hypothesis testing program which relies on the specialized databases of gene/protein interactions for identifying potentially undiscovered members of multigene families through comparisons of regulatory networks for different species and testing hypotheses with regard to regulatory cascades. A comparison of homologous regulatory networks within the same organism and between different species of organisms will allow the identification of genes absent in one of the systems under comparison, thus providing a set of candidate genes. In this way, genes that contribute to the phenotype of a specific disease associated with a particular biological system under analysis may be identified, mapped and subjected to mutational analysis and functional studies.

4. BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a block diagram illustrating the three major programs of the method according to the present invention: (i) the generation of specialized databases based on information on gene/protein structure, function and regulatory interactions derived from research papers and databases; (ii) sequence analysis; and (iii) simulation and hypothesis testing;

Figure 2 is a block diagram of an information extraction system in accordance with a preferred embodiment of the present invention;

Figure 3 is a diagram illustrating the object representation of molecules and relations between them;

Figure 4 shows a set of keywords defining proteins involved in apoptosis pathways, these keywords having been utilized for generating a specialized sequence database Apoptosis3, this list having been compiled manually for testing the concept of specialized databases;

Figure 5 shows a "species tree," which is a graph depicting the correct order of speciation events leading to a set of present day species; a "gene tree," which

is a graph depicting a history of a few genes from the same species, where each species can be represented by multiple paralogous genes (because the set of known genes is incomplete for most genomes, and there are often multiple representations of the same gene family in the same genome, the gene tree can be drastically different from the corresponding species tree); and a "reconciled tree", which is the gene tree that would be obtained if gene deletions were completely forbidden and all genes were known for all species under analysis;

Figure 6 shows the original tree of ALDH sequences, indicating sequence clusters where bacterial, plant, fungal and nematode orthologous genes are present, but a human ortholog was not yet known;

Figure 7 shows the same phylogenetic tree as in Figure 6 with an additional human protein, referred to as antiquitin which was discovered by the method of the invention;

Figure 8 is a schematic diagram illustrating functional network-based gene discovery in accordance with the present invention;

Figure 9A presents diagrams depicting the regulatory relationships among hypothetical proteins (denoted with Arabic numerals) of hypothetical species A and B. Proteins in different species denoted with the same numeral are considered orthologous. The diagrams show that regulatory relationships between a pair of proteins can be of three different kinds;

Figure 9B, 9C, and 9D are diagrams representing Boolean operations OR, AND, and XOR, on arcs of the two oriented graphs of Figure 9A, the same operations being applicable to the set of vertices of the two oriented graphs;

Figure 10 is a diagram representing a hypothetical example of defining homologous protein networks in two different species using protein motifs, the diagram showing only two hypothetical proteins (1 and 2) for species A and three hypothetical proteins (1, 3, and 4) for species B. Protein 1 in both species has motifs α and β, protein 2 has motifs δ, ϵ, and ζ, and proteins 3 and 4 have motifs δ and ζ, and ϵ, respectively. The motif analysis can indicate that proteins 3 and 4 in species B may collectively perform the same function as protein 2 in species A;

Figure 11A and 11B are diagrams respectively representing hypothetical examples of evaluating the impact of a "knockout" of hypothetical gene A on the expression of a hypothetical gene B. The effect of knock-out of gene A calculated by multiplication along the shortest pathway connecting genes A and B is inhibition of gene B, the resulting effect being zero if the orientation of only one arc in the same pathway is reversed;

Figure 12 is a flow chart representing the scheme of gene discovery analysis involving motif/domain analysis in accordance with the present invention; and

Figure 13 Identification of genes in *C. elegans* containing either POZ or kelch domains. The protein excession numbers are indicated adjacent to the different protein domains. The protein corresponding to accession number gi/1132541 contains a POZ domain, death domain, kinase domain and heat repeat.

Figure 14A. Two human sequences with the closest homology to the *C. elegans* sequence gi/1132541.

Figure 14B. Computed gene tree indicating that the identified human gene represents an ortholog of the *C. elegans* gene gi/1132541.

Figure 14C. Nucleotide sequence of the death domain gene.

Figure 14D. Deduced amino acid sequence of the death domain protein.

Figure 15. Identification of candidate gene implicated in the etiology of Chronic Lymphocytic Leukemia (CLL). Sequence homology between a CLL region open reading frame and mouse Rpt1 (sp/P15533/RPT1) is presented.

Figure 16A-B. Model of regulatory functions of Rpt1. Figure 16A indicates that in mouse T lymphocytes Rpt1 serves as a repressor of the gene for interleukin 2 receptor (IL-2R). Figure 16B demonstrates that when Rpt1 is knocked out, the regulatory effect is manifested as a block of the apoptotic pathway for T-lymphocytes resulting in accumulation of T-lymphocytes in blood.

Figure 17A. Two EST sequences identified by searching a protein dbEST using the mouse Mad3 protein as a query.

Figure 17B. Nucleotide sequence of the human Mad3 gene.

Figure 17C. Complete sequence of the human Mad3 protein. A search was conducted to identify overlapping sequences. The complete sequence of the gene was assembled and the amino acid sequence deduced. The translated human Mad3 sequence consists of 206 amino acid residues 81% of which are identical to the mouse Mad3 protein.

Figure 17D. Multiple alignment of the human Mad3 amino acid sequence with known Mad proteins.

Figure 18A. Phylogenetic tree indicating relationship between three known mouse Mad genes and their two human homologs.

Figure 18B. Phylogenetic tree including new human Mad3 sequence. The phylogenetic tree indicates that the new human gene belongs to the family of Mad proteins and is an ortholog of mouse Mad3.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention provides methods for identification of novel genes comprising: (i) generating specialized databases containing information on gene/protein structure, function and regulatory interactions and, (ii) sequence analysis which includes homology searches and motif analysis thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The specialized databases are constructed utilizing information concerning gene/protein structure or function derived from unpublished data, research articles and/or existing databases. The specialized databases can be used to identify novel genes by: (i) searching for motif/domain combinations characteristic for a putative gene of interest; (ii) phylogenetic tree analysis of homologous genes for predicting the existence of yet undiscovered genes; (iii) comparing members of interactive gene/protein networks from different species for predicting the existence of yet undiscovered genes; and (iv) testing a hypothesis with regard to known interactions of homologs from other species in regulatory pathways.

5.1. THE NATURAL LANGUAGE PROCESSING

The present invention relates to a natural language processing system that is designed to parse the electronic versions of articles published in journals that report on structural interactions among genes and proteins. The system provides a method for extracting information on interactions among genes and proteins, their domain/motif structure, and/or their sub-cellular and tissue expression/distribution patterns, followed by computer representation of such information.

The general natural language-processing system of the invention is schematically depicted in Figure 2. The collection phase automatically collects articles from appropriate literature, and selects articles that contain relevant information using Keyword search techniques. In the next phase, the preprocessor standardizes the selected articles so that they consist of tagged ASCII text where the tags delineate critical components of the article. The next phase, termed the extraction phase, retrieves and classifies biological entities, *i.e.*, as names of proteins, genes and small molecules. In addition, the relationship extraction phase recovers structural relationships between the entities. This phase is followed by a phase which performs an analysis of the sequence of events.

The final phase of the system processes the output extracted from an article to remove redundancies, inconsistencies and to incorporate implicit information before adding the extracted knowledge consisting of biological entities, their attributes, conditional constraints, and relationships between them, for subsequent use in analysis and hypothesis testing. The information extraction system as depicted in Figure 2, referred to herein as "GENIE," is designed for use as a general processor within the domain of genomics literature although the system may also be used in other specialized domains. GENIE is an adaptation of MedLEE developed for the medical domain. GENIE uses the same source code as MedLEE but the Lexicons and grammar were adapted for genomics literature.

The information extraction system of the present invention is described below, by way of example, with reference to the genomics domain uses of GENIE. It is written in Quintus Prolog and uses the Unix or Windows operating systems, as described in detail below.

A natural-language phrase included in text document is understood as a delimited string comprising natural-language terms or words. The string is computer readable as obtained, *e.g.*, from a pre-existing database, a keyboard input, optical scanning of typed or handwritten text, or processed voice input. The delimiter may be a period, a semicolon, an end-of-message signal, a new-paragraph signal, or any other suitable symbol recognizable for this purpose. Within the phrase, the terms may be separated by another type of delimiter such as a blank or another suitable symbol.

As a result of phrase parsing, terms in a natural-language phrase are classified, (*e.g.*, as referring to a gene, a protein, or their interactions) and the relationships between the interactions are established and represented in a standard form. For example, in the sentence "Rap inhibited fyn", the structured form would be:

[action,inactivate,[protein,rap],[protein,fyn]].

In such an example, the interaction is "inactivate", the agent is "Rap" and the target is "fyn." More complex sentences consisting of nested relationships, such as "The activation of BAD was suppressed by the phosphorylation of JNK" can also be parsed and represented appropriately. The structured output form for this sentence would be: [action,inactivate,[action,phosphorylate,x,[protein,jnk],[action,activate,x,[protein,bad]]

In the first example, the primary interaction is "inactivate"; in the second example, an interaction "phosphorylate" is the agent where the protein "jnk" is its target (the agent of "phosyphorylate" in not specified and thus is represented as "x"). In this example, the target of "inactivate" is also an interaction "activate" where the target is the protein "bad" and the agent is unknown.

While parsing is based on both syntactic and semantic grammatical patterns, the substances in a domain are normally only semantic categories such as "protein", "gene", and "small molecule." There are no corresponding syntactic categories needed for these substances because they are normally all nouns. However, each action can be categorized both semantically and syntactically. An action, which is a semantic category, can generally occur syntactically as a verb "inactivate" or as a noun "inactivation." Therefore there are two sets of lexical entries for the actions:

syntactic and semantic. The syntactic lexicon for actions specifies the main syntactic category such as "v" for verb, "ving" for progressive form of verb, and "activation" for noun. The semantic entries for actions not only categorize the actions, but also specify features for each action. For example, one feature provides the number of arguments that are expected for the action, *i.e.*, some actions are associated with two arguments because they have an agent and a target as "inactivate", and others just have an agent "mutate." The lexicon of substances and structures appears as Appendix A; the syntactic lexicon for actions appears as Appendix B; and the semantic lexicon of actions appears as Appendix C.

A second feature specifies whether or not the arguments should be reversed when obtaining the target form. For example the arguments of "attributable to" should be reversed, *i.e.*, in "the phosphorylation of jnk is attributable to the activation of bad", the underlying action is "cause" (from "attributable to"), the agent is the "activation of bad" and the target is "the phoshorylation of jnk"), whereas the arguments of "activates" is not(i.e. in "jnk activates bad" , the agent is "jnk" and the target is "bad").

Figure 2 shows a preprocessor module of GENIE by which natural-language input text is received. The preprocessor thus performs lexical lookup to identify and categorize multi-word and single word phases within each sentence. The output of this component consists of a list of word elements where each element is associated with a word or multi-word phrase in the report. For example, assuming that the sentence "bad functions as a negative regulator of the activation of jnk" is at the beginning of the report, it would be represented as a list of elements where each element is a word or phrase. For example, element 1 is associated with "bad", element 2 with the multi-word phrase "functions as a negative regulator of", element 8 with "the", and element 9 with "activation". The remainder of the list of word positions would be associated with the remaining words in the report. Some of the phrases may not need lexical lookup because they already have been tagged by a previous component. Such a tagging system is described below in Section 5.2.

The second component of the GENIE system is the parser. It utilizes the grammar and categories assigned to the phrases of a sentence to recognize well-

formed syntactic and semantic patterns in the sentence and to generate structured output forms. The parser proceeds by starting at the beginning of the sentence element list and following the grammar rules. When a semantic or syntactic category is reached in the grammar, the lexical item corresponding to the next available unmatched element is obtained and its corresponding lexical definition is checked to see whether or not it matches the grammar category. If it does match, the word or phrase is removed from the unmatched sentence list, and the parsing proceeds. If a match is not obtained, an alternative grammar rule is tried. If no analysis can be obtained, an error recovery procedure is followed so that a partial analysis is attempted. The actual grammar used for GENIE appears as Appendix D.

The parser module of GENIE uses the lexicon, and a grammar module to generate target forms. Thus, in addition to parsing of complete phrases, subphrase parsing can be used to an advantage where highest accuracy is not required. In case a phrase cannot be parsed in its entirety, one or several attempts can be made to parse a portion of the phrase for obtaining useful information in spite of a possible loss of information.

Conveniently, each module is software-implemented and stored in random-access memory of a suitable computer, *e.g.*, a work-station computer. The software can be in the form of executable object code, obtained, *e.g.*, by compiling from source code. Source code interpretation is not precluded. Source code can be in the form of sequence-controlled instructions as in Fortran, Pascal or "C", for example. Alternatively, a rule-based system can be used such a Prolog, where suitable sequencing is chosen by the system at run-time.

An illustrative portion of the GENIE system is shown in the Appendix D in the form of a Prolog source listing with comments. The following is further to the comments.

Process_sents with *get_inputsents, process_sects* and *outputresults* reads in an input stream, processes sections of the input stream according to parameter settings, and produces output according to the settings, respectively. Among parameters supplied to *Process_sents* are the following: Mode (specifying the parsing

mode) and Protocol (html or plain). *Process_sents* is called by another predicate, after user-specified parameters have been processed.

The parsing modes are selected by GENIE so as to parse a sentence or phrase structure using a grammar that includes one or more patterns of semantic and syntactic categories that are well-formed. For example, for the phrase "bad inactivates jnk", a legitimate pattern can be substance1 action substance2, wherein substance1 = protein bad, action = "inactivates" and substance2 = "jnk." However, if parsing fails, various error recovery modes are utilized in order to achieve robustness. The error recovery techniques use methods such as segmenting the sentence, processing large chunks of the sentence, and processing local phrases. Each recovery technique is likely to increase sensitivity but decrease specificity and precision. Sensitivity is the performance measure equal to the true positive rate of the natural language processing, *i.e.*, the ratio of information extracted by the natural language processing system that should have been extracted. Specificity is the performance measure equal to the true negative information rate of the system, *i.e.*, the ratio of information not extracted by the NLP system that should not have been extracted. Precision is the reliability of the system, *i.e.*, the ratio of information extracted correctly compared to all the information that was extracted. In processing a report, the most specific mode is attempted first, and successive less specific modes are used only if needed.

In accordance with the preferred embodiments of the present invention, the parser of Figure 2 includes five parsing modes, Modes 1 through 5, for parsing sentences or phrases. Nominally, the parser is configured to first select Mode 1. If Mode 1 is not possible, the program continues with Mode 2 and so forth until parsing is complete. With Mode 1, the initial segment is the entire sentence and all words in the segment must be defined. This mode requires a well-formed pattern for the complete segment.

Mode 2 requires that the sentence or phrase be segmented at certain types of words or phrases, *e.g.*, " is attributable to." Here, an attempt is made to recognize each segment independently, *i.e.*, a first segment ending with the word "is" and a second segment beginning with the word after "to." The segmenting process is

repeated until an analysis of each segment is obtained or until segmenting is no longer possible.

Mode 3 requires a well-formed pattern for the "largest" prefix of the segment, *i.e.*, usually at the beginning of the segment. This occurs when a sentence contains a pattern at the end which is not in the grammar but a beginning portion that is included. For example, in "bad inactivates jnk at this time", the beginning of the sentence "bad inactivates jnk" will be parsed and the remainder will be skipped.

Mode 4 requires that undefined words be skipped and an analysis be attempted in accordance with Mode 1. Mode 4 is useful where there are typographical errors and unknown words. For example, in the phrase "abc bad inactivates jnk", the word *abc* is unknown to the system and will be ignored but the remainder of the phrase will be parsed.

Mode 5 first requires that the first word or phrase in the segment associated with an action be found. Next, an attempt is made to recognize the phrase starting with the leftmost recognizable argument. For example, in "during bad inactivates jnk on the fifth day," the phrase "bad inactivates jnk" will be parsed and the remaining words will not be. If no analysis is found, recognition is retried at the next possible argument to the right. This process continues until an analysis is found.

Process_sects with *get_section* and *parse_sentences* gets each section and generates intermediate output for the sentences in each section.

Write produces the output as a list consisting of relations and interactions

Setargs sets arguments or parameter values based on user input or by default.

The structured output generated by the GENIE program uses a frame-based representation. Each frame specifies the informational type, the value, and arguments or modifier slots which are also frames. Consider the text data input "bad inactivates the phosphorylation of jnk." A corresponding output, as shown below, is a frame denoting an action, which has the value inactivate; in addition, there are two arguments. The first argument is a protein bad and the second argument is an action with the value phosphorylate, which has two arguments. The first argument is x

signifying that the agent has not been specified; the second argument is a protein with the value jnk. The second argument is the target:

[action,inactive,[protein,bad],[action,phosphorylate,x,[protein,jnk

In summary, a computer system has been disclosed that generates structured information concerning protein and gene interactions and relationships.

5.2. USE OF BLAST FOR FINDING GENE AND PROTEIN NAMES IN JOURNAL ARTICLES

In a specific embodiment of the invention, an exhaustive list of gene and protein names, extracted from GeneBank, is translated into a different alphabet system by substituting each character in the name with a predetermined unique nucleotide combination. The encoded names are then imported into the BLAST database using the FASTA format. The scientific journals are translated, using the same nucleotide combinations, into a continuous string of nucleotides. A query is then used to match the translated journals against the nucleotide representation of gene and protein names in the BLAST database. Significant alignments associated with gene and protein names are listed in the BLAST output file, which is subsequently processed using Perl-scripts. The final result consists of the original journal article with XML tags surrounding the gene and protein names.

To adapt the problem to BLAST's statistical foundation, different measures were undertaken to limit the output to the most relevant gene and protein names. In addition, in order to fine-tune the matching process, different BLAST parameters were adjusted, such as the *word size* (which sets the size of the high scoring words, thus influencing the sensitivity of finding HSPs) and *mismatch penalty* (exact vs approximate matching).

In a specific embodiment of the invention, gene and protein names are extracted from GeneBank's gene symbol index file. The following is an excerpt of the file after discarding entries that are either composed of only numbers or of less than two alphabetic letters:

gfap gamma

hox a10

hox a1
wac 3'-end
pit-1/ghf-1 variant
[...]

This list of gene and protein names is translated into a different alphabet system by substituting each character in the name with a predetermined unique nucleotide combination. The conversion chart is listed in Appendix E. The encoded names are then imported into the BLAST database using the FASTA format. For example, the first entry in the list above is "gfap gamma." After translation using the conversion chart, the same name appears as follows:

AGCAACTAAACACCCATCCAAGCAAACACACACACAAAC

Thus, the complete FASTA entry looks like this:

>gi|1 species,gp,gfap gamma
AAGCAACTAAACACCCATCCAAGCAAACACACACACAAAC

In FASTA, the definition line (marked with '>') contains information about the database entry. This line can contain any kind of information. The information important for this particular example is the third entry in the definition line, 'gp', that specifies that the name can represent a gene *or* a protein. If the name is unambigous, then the definition line states that the name is only associated with a gene ('g') or protein ('p'). The fourth entry in the definition line is the name of the protein or gene, "gfap gamma" in this case.

The second line in the FASTA format normally contains the actual sequence of the protein/gene. In the example presented, the second line contains the translated protein or gene name.

All gene and protein names are translated into the nucleotide representation and converted into the FASTA format. Then, the database containing these FASTA entries are specially compiled for use in BLAST queries using a program that is included in the BLAST package called "formatdb".

Thus, the scientific journals are translated, using the same nucleotide combinations, into a continuous string of nucleotides. For example, the sentence "In

the absence of costimulation, T cells activated through their antigen ..." is translated into

"AAGTACAGATCCACGGAAGGAACGATCCAAACAAAGACGCAACGACAG
AAATAACGATCCACATAACTATCCAAATACATACGCACGGAAGTACACAC
GTAATTAAACACGGAAGTACATACAGATCCATCCACGGATCCAAATAACG
AATTAATTACGCATCCAAACAAATACGGAAGTACTCAAACACGGAACGAA
CCATCCACGGAAGGACCTACATACGTAAGCAAGGATCCACGGAAGGAAC
GAAGTACCTATCCAAACACAGACGGAAGTAAGCAACGACAGATCC "

A query is then used to match the translated journals against the nucleotide representation of gene and protein names in the BLAST database. The query is executed using the blastall program that is included in the BLAST package. The query line looks like:

blastall -p blastn -d FASTA.dat -i query.txt

The flag 'p' denotes the sub-program (blastn is a sub-program of blastall that performs nucleotide matches), 'd' denotes the file that contains the FASTA entries and 'i' denotes the translated query text.

Significant alignments associated with gene and protein names are listed in the BLAST output file. This is an excerpt from a BLAST output file:

gi|63624 species,gp,ner
Length = 12
Score = 24.4 bits (12), Expect = 3e-05
Identities = 12/12 (100%)
Strand = Plus / Plus
Query: 729 acagaacgacct 740
Sbjct: 1 acagaacgacct 12

The first line denotes the database entry. The second line denotes the database sequence length, followed by the alignment score and the E-value. The next line indicates paired matches, mismatches and gapped alignment (the latter two are not shown in this example). The lines 'Query' and 'Sbjct' show the actual alignment between the query and database sequence. This output file is subsequently processed

using a Perl-script (see Appendix F). The script shown in Appendix G scans the output file, which is sometimes several megabytes long, for any segments that start at position 1 of the database sequence (thus disregarding any segments that are only part of the sequence). In addition, the script allows for 10% mismatches between the aligned sequences for long sequences (as shown in the script of Appendix E), or 0% mismatches for short sequences. After scanning the output file, an intermediary file that lists the candidate sequences is created:

tran|365|381|gp|18493
tran|1|17|gp|18493
peci|549|565|gp|58106
il-2|621|637|gp|82396
il-2|325|341|gp|82396
gati|193|209|gp|92088
prod|641|657|gp|52292
rap1|105|121|gp|49898
spec|545|561|gp|33183
crip|385|401|gp|118905
crip|21|37|gp|118905
as|161|177|gp|133961
her|65|77|gp|88411

The intermediary file lists the name of the sequence, followed by the starting and end point in the query sequence (corresponds to where the two sequences matched), the semantic class of the name (protein, gene or protein/gene). The last number is not considered.

The intermediary file is then scanned by another Perl program (Appendix G). This program compares the starting end points with the actual text, making sure that the matched name is an 'autonomous' entity in the query text. For example, while "per" in " per gene" should be recognized as a gene name, "per" in "personal" should not be recognized as a gene name. The program recognizes other characters than the space character delimiting an 'autonomous' gene or protein name.

In addition, the script looks for plurals of words. For example, " interleukins" should be recognized as a protein name, although only the singular form, "interleukin", is in the database.

The final result consists of the original journal article with XML tags surrounding the gene and protein names. This is done using the same script as in Appendix G:

blocked <phr sem="gp">T cell antigen receptor</phr> (TCR)- and <phr sem="gp">CD28</phr>-mediated <phr sem="gp">IL-2</phr> gene transcription. Therefore, <phr sem="gp">Rap1</phr> functions as a negative regulator of...

To adapt the problem to BLAST's statistical foundation, different measures were undertaken to limit the output to the most relevant gene and protein names.

BLAST is sensitive to the search space the program works in. Thus, given a long query sequence and a large sequence database, matches have a lower statistical significance because the chances are higher that the matches could have occurred by chance alone. In addition, matches with few letters have a lower statistical significance than matches with many letters. In order to find all true matches with any significance level, some measures were undertaken to address this problem. For example, (i) the query sequence was divided into 10 equal length parts, *i.e.*, the journal article was divided into 10 parts and 10 different queries are run on each part separately; (ii) the sequence database (with the gene and protein names) is separated into 5 databases, each containing protein/gene names of different length; (iii) gene and protein names with less than 3 letters in the database were 'expanded', *i.e.*, spaces were added at the beginning and the end of the name. Doing so, the statistical significance of a match containing a short name was higher. A space does not only include an empty character. For example, a gene name "k4" could occur in a journal article as "kinin 4 (k4)". It was therefore important to define several characters as substitutes for a space character. The alphabet in Appendix E defines the nucleotide combination ATCC as such a substitute.

Working with nucleotides implies that errors involving reading frames must be addressed. For example, working with a code of four letters, the nucleotide combination ATCTGTCACG could mean ATCT/GTCA or TCTG/TCAC or CTGT/CACG . Since the text is translated into a nucleotide combination, only one of these possibilities is correct. But BLAST can not distinguish between these solutions, *i.e.*, BLAST would potentially match a database sequence to a wrong reading frame in the query sequence, producing many nonsense results that could compromise the significance of true results.

The solution to this problem is a comma-free code. A comma free code knows only one correct reading frame. BLAST therefore does not produce any nonsense results. A comma-free code consists of only one permutation of a nucleotide combination. For example, given the nucleotide combination ATCC and its permutations CATC, CCAT and TCCA, only ONE of these permutations would be included in a comma-free code. The code in Appendix E does represent a comma free code. Comma-free codes were discussed in the early days of DNA research (Crick et al., Proc. Natl. Acad. Sci. 43:416-421).

In order to fine-tune the matching process, different BLAST parameters must be adjusted, for example: *word size* (which sets the size of the high scoring words, thus influencing the sensitivity of finding HSPs);*mismatch penalty* (exact vs approximate matching); *numbers of alignments to show* (true matches of low significance can sometimes be at the very end of the BLAST output, therefore many alignments have to be shown); and *expectation value* (which sets the significance value for matches in the output file).

5.3. GENERATION OF SPECIALIZED DATABASES

In accordance with the present invention, specialized databases may be developed that contain information derived from unpublished data, publications such as research articles, theses, posters, abstracts, etc. and/or databases concerning interactions among genes and proteins, their domain/motif structure, and their biological functions.

For example, but not by way of limitation, a specialized database may be prepared as follows. Protein and gene sequences may be provided, for example, by the Java program PsiRetrieve which allows for quick retrieval of protein or nucleotide sequences from binary BLAST databases by sequence accession number, keyword or groups of keywords, or species name. In addition, using the program PsiRetriever, sequences encoding the proteins of interest may be retrieved from the non-redundant (NCBI) database of protein sequences and stored as a FASTA file. The FASTA file is then converted into a binary blast database using the program FORMATDB from the BLAST suit of programs.

Known motifs/domains for proteins may also be collected using the flat file versions of major protein databases, such as SwissProt (http://expasy.hcage.ch/sprot) and the non-redundant database of NCBI (http://www3.ncbi.nlm.nih.gov). The databases can be downloaded and searched for the keywords "motif" and "domain" in the feature tables of proteins. In addition, existing databases of motifs and domains, such as BLOCKS (http://dupsas.Weizmann.ac.il/bcd/bcdparent//databanksblocks/hfml) and pfam(http://www.sanger.ac.uk//software/pfam; http://pfm.wustl.edu), can be downloaded (Henikoff et al., 1991, NAR 19:6565-6572). Still further, it is understood that any publically available database containing gene/protein sequences may be utilized to generate the specialized databases for use in the practice of the present invention.

Homologous sequences may be aligned using, for example, the CLUSTALW program (Higgins, et al. 1996 Methods in Enzymology 266: 383-402). A protein's sequence corresponding to each domain/motif can be identified, saved and used for building a Hidden Markov Model (HMM) of the domain/motif using a HMMER and HMMER2 packages (see, Durbin, R. et al. 1998 in Biological Sequence Analysis: Probablistic Models of Proteins and Nucleic Acids). HMMER and HMMER2 packages are useful for (i) building HMMs from sets of aligned protein or nucleotide sequences, and (ii) comparing the HMMs with sequence databases aimed at identifying significant similarities of HMMs with database sequences. Both nucleotide and protein databases can be used for this purpose. Alternatives to the

Hidden Markov Model method for building domain/motif models include neural network motif analysis (Wu, C.H. et al., 1996, Comput Appl Biosci 12, 109-18; Hirst, J.D., 1991, Protein Eng 4:615-23) and positional weight matrix analysis (Claverie, J.M., 1994, Comput Chem 18:287-94; Venezia, D., 1993, Comput Appl Biosci 9:65-9; Bucher, P. 1996, Comput Chem, 20:3-23; Tatusov, R.L., 1994, Proc Natl Acad Sci USA 91:12091-5).

Once a comprehensive collection of motifs/domains is created, each particular protein may be compared against a complete database of HMMs to identify known motifs and domains.

The Hidden Markov Model (HMM) is built using the following steps:

A1. Start with a motif/domain name and a single amino acid sequence representing a domain or motif.

A2. Do PSI-BLAST (BLASTPGP) search with the motif/domain sequence against a protein non-redundant database.

A3. Retrieve the sequences identified in the database search from the protein sequence database. Exclude low-complexity sequences, short or incomplete sequences and sequences with similarity score above a selected threshold of PPD value <0.001

A4. Align the set of sequences with CLUSTALW (or other multiple sequence alignment program).

A5. Use the set of aligned sequences for building HMM with the programs provided with HMMER and HMMER2 packages (see Hughey and Krogh 1996, J. Mol. Biol. 235:1501-1531).

A6. Do a new database search comparing new HMM with the non-redundant protein database.

A7. Continue steps A3-A6 until the convergence of the Markov model *i.e.*, until no new sequences are identified, or the maximum allowed number of iterations as defined by the user is reached. (Hugh R. and Krogh A., 1996, Comput. Appl. Biosci. 12: 95-107).

In addition, in yet another embodiment of the invention, a specialized database may be designed to contain a semantic model of proteins and of the possible

interactions between them. Such databases are particularly useful for computation and analysis of regulatory networks between proteins. The semantic model is designed for representing substances, such as proteins and actions between them, and is based on widely accepted principles of object-oriented programming languages such as Java. Figure 3 is a diagram illustrating the object representation of molecules and relations between them. As indicated in Figure 3 there are six major classes, corresponding to the top-level classification of objects and actions: (*i*) a substance; (*ii*) a state of a substance; (*iii*) a similarity between substances; (*iv*) an action between substances; (*v*) a result of the action; and (*vi*) a mechanism that enables an action.

Figure 3 presents the class design graphically, listing the variables that represent the properties of each class or class object in the implementation. Classes can be made nested via the mechanism of "inheritance", *i.e.*, classes are defined starting with the most general ones and moving towards more specific classes. Definition of more specific classes is simplified because the properties of the general classes are "inherited" by the specific classes and need not be redefined each time (see, Flanagan 1997, Java in a Nutshell, Second Edition. O'Reilley & Associates, Inc. Sebastopol, CA).

As shown in Figure 3, the two key object types in this scheme are substances (nodes of the graph representing regulatory networks) and actions (oriented edges connecting pairs of nodes), while result and mechanism objects are auxiliary to object action. Each substance object is characterized with a state. In this scheme, action is the most complicated object; each action object is characterized by a specific pair of substances participating in the action, one of which can be active and is referred to as Subject Substance and the second of which can serve as a substrate for the former and is referred to as Object Substance. Furthermore, for each action the initial and final states corresponding to interacting substances are defined. The property Time Required of each Action Object allows the setting of different durations for different actions (time is measured in relative units; see René Thomas and Richard D'Ari, 1990, "Biological Feedback," CRC Press Boca Raton, Ann Arbor, Boston).

Once developed, the specialized databases can be used to identify novel genes based on computation and analysis of phylogenetic trees for multigene families and analysis of homologous regulatory networks.

In a specific embodiment of the invention, a specialized database was generated using a set of keywords defining proteins involved in apoptosis (see, Figure 4). The specialized sequence database was referred to as Apoptosis 3. As a first step in generating the specialized database, a comprehensive set of articles describing the system of apoptosis or programed cell death was compiled. The articles were analyzed and information on regulatory pathways characterizing apoptosis from a variety of different organisms was extracted. Such pathways included those involved in MHC-T cell receptor interactions, inflammatory cytokine signal transduction, induction by light, γ-radiation, hyperosmolarity or heat shock, pathways involving immunoregulatory receptors or receptors having cytoplasmic domains, integrin-related pathways and perforin/granzymeβ related pathways. The collected information was stored using Powerpoint (Microsoft) as a collection of graph/plots depicting the regulatory pathway. In addition, a list of proteins relevant to regulation of apoptosis was compiled.

Using the program Psi Retriever, sequences encoding the proteins relevant to regulation of apoptosis were retrieved from the non-redundant (NCBI) database of protein sequences and stored as a FASTA file. The FASTA file was then converted to a binary blast database using the program FORMATDB from the BLAST suit of programs. The BLAST suit of programs provides a set of programs for very fast comparisons of a single sequence to a large database. Both the database and the search or query sequence can be any combination of nucleotide and/or amino acid sequences.

In a working example described herein, the Apoptosis 3 database was used to compare genomic and cDNA sequences derived from the 13q region of human chromosome 13. This region of the chromosome is associated with Chronic Lymphocytic Leukemia (CLL). Using this method of analysis a human gene with significant homology to the mouse Rpt1 gene was identified. When the activity of Rpt1 is knocked out in mice, the regulatory effect is manifested as a block in T-

lymphocyte apoptosis. This result indicates that the identified human Rpt1 homology may represent the gene in which genetic defects lead to CLL.

The amino acid sequence of the human Rpt1 gene is presented in Figure 15. The present invention relates to nucleic acid molecules encoding the human Rpt1 protein shown in Figure 15. The invention also relates to nucleic acid molecules capable of hybridizing to a nucleic acid molecule encoding the human Rpt1 protein presented in Figure 15 under conditions of high stringency. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50 mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C in prehybridization mixture containing 100mg/ml denatured salmon sperm DNA and 5-20 x 10^6 CpM of ^{32}P-labeled probe. Washing of filters is done at 37°C for 1 h in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1 x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.4. GENE DISCOVERY THROUGH PHYLOGENETIC ANALYSIS OF GENE FAMILIES

The present invention provides a method for identifying novel genes comprising the following steps: (i) comparing a single sequence with a database; (ii) processing the output into a sequence alignment; (iii) computing gene trees; and (iv) analyzing the trees to predict the existence of undiscovered genes.

Figure 5 shows a "species tree," a "gene tree" and a "reconciled tree". A "species tree", as defined herein, is a graph depicting the correct order of speciation events leading to a set of present day species as defined by taxonomy. A "gene tree" is a graphical representation of the evolution of a gene from a single ancestral sequence in a common progenitor to a set of present-day sequences in different species. Where gene duplication has occurred, a branch is bifurcated. The branch lengths of a gene tree are most frequently measured either in terms of the number of

amino acid or nucleotide replacements per site or in terms of millions of years (absolute geological time). In the former case, the average replacement rate in the majority of the published trees varies among tree branches, and the root-to-tip distances are different for different present day sequences. In the latter case, all root-to-tip distances are equal and the height of each interior node of the tree corresponds to the absolute geological time passed since the gene duplication corresponding to the interior node took place.

If a gene is unique, *i.e.*, represented with a single copy per genome rather than being a member of a family of similar genes, the correct gene tree depicting the origin of this gene in a few different species is identical to the species tree. In many instances, a single ancestral gene has been duplicated repeatedly during evolution to form a multigene family. A gene tree is constructed from a gene as it occurs in several species and reflects both speciation events and gene duplications within the same genome. Two homologous genes taken from different species that originated from the nearest common ancestor by speciation are referred to as orthologs, while any two genes that originated from the common ancestor via a series of events involving intragenomic duplications, or conversions, are called paralogs. The terms "ortholog" and "paralog" are applied to both nucleic acid and proteins herein.

If gene deletions are forbidden and all genes for all species represented in the tree are known, the gene tree can be reconfigured to recapitulate the species tree, such that each subtree contains only orthologous genes. This tree is referred to as a reconciled tree and is shown in Figure 5. Imperfect gene trees which contain incorrect or partial species subtrees can be used to build reconciled trees that indicate events of speciation, gene loss, and gene duplication.

Orthologs from different species in gene trees are usually clustered together, so that if all the existing homologous genes from different species were known, the same relationship of species would be recapitulated in each cluster of orthologous genes. Since in reality a considerable number of genes are not yet identified, the real gene trees contain incomplete clusters of orthologs that can be used for identification of the missing genes.

By applying phylogenetic analysis, *i.e.*, reconstruction of gene trees of gene/protein sequences, one can predict the existence of undiscovered genes in humans and other species in addition to identifying the function of a gene. Such a technique is a significantly more powerful tool for identification of new genes than mere sequence comparisons.

Methods of computing gene trees from a set of aligned sequences include the : (i) heuristic method based on an optimization principle which is not directly motivated by a probability model (Fitch, 1974 J. Mol. Evol. 3:263-268)), (ii) the maximum likelihood method (Goldman, 1990, Syst. Zool. 30:345-361; Yang et al., 1995, Syst. Biol. 44:384-399; Felsenstein, J., 1996, Methods Enzymol. 266-418-427); and (iii) the distance matrix tree making method (Saito, N. and Nei, M., 1987, Mol. Biol. Evol. 4:406-425). Since the data analyses of orthologs and paralogs often involve very distantly related sequences, the maximum likelihood method is preferably used for small data sets and the distance-matrix method in other instances.

To construct a reconciled tree according to the invention, the first step comprises a search for homologs in a publicly or privately available database such as, for example, GenBank, Incyte, binary BLAST databases, Swiss Prot and NCBI databases. Following the identification of homologous sequences a global alignment is performed using, for example, the CLUSTALW program. From the sequence alignment a gene tree is constructed using, for example, the computer program CLUSTLAW which utilizes the neighbor-joining method of Saito and Nei (1997, Mol. Biol. Evol. 4:406-425). Construction of a species tree is then retrieved from, for example, the following web site:
http://www.3.NCBI.NLM.NIH.GOV//taxomy.tax.html.

The species tree and gene tree are given as input into the algorithm described below, which integrates both trees into a reconciled tree. Agreement between the gene tree and the corresponding species tree for any given set of sequences indicates the identification of orthologs. In contrast, disagreement between the species and gene tree suggest a gene duplication that resulted in the formation of a paralog. Thus, through generation of a reconciled tree one can identify orthologs present in one species but missing in another. These can be deduced by forming

subtrees of orthologs in a gene tree, and then comparing the subtree in the gene tree with a species tree. A missing gene appears as a branch present in the species tree but absent in the gene tree. The algorithm for defining an orthologous gene subtree and predicting the undiscovered, or lost in evolution, genes is as follows:

Let T_g be the most likely gene tree identified with one of consistent tree-making methods from a set of properly aligned homologous genes {1, 2, ..., s}, such that one or more homologous genes from every species corresponds to pending vertices of T_g. Each gene is labeled with the species it comes from (1,...,s) adding subscripts to distinguish homologous genes from the same species whenever it is necessary. Let T_g be the true species tree (tree correctly reflecting speciation events which we assume to be known) for species {1, 2, ..., s}. Due to the biological meaning of T_s each species in this tree is represented only once. It is assumed that both T_s and T_g are binary, although it is straightforward to extend the algorithm described here to the case of multifurcated trees.

Algorithm

A1. For each pair of interior nodes from trees T_g and T_s, compute similarity $\sigma(S_{gi},S_{sj})$.

A2. Find the maximum $\sigma(S_{gi},S_{sj})$.

A3. Save S_{gi} as a new subtree of orthologs, save $\{S_{gi}\}$ - $\{S_{sj}\}$ as a set of species that are likely to have gene of this kind (or lost it in evolution).

A4. Eliminate S_{gi} from T_g; $T_g := T_g \backslash S_{gi}$.

A5. Continue A2 - A4 until T_g is non-empty.

The following definitions apply:

Let S_{gi} be an *i*th subtree of T_g (corresponding to the *i*th interior node), correspondingly, let S_{sj} be *j*th subtree of tree T_s.

Let $\{S_{gi}\}$ stand for an unordered set of species represented in S_{gi} such that each species is represented exactly once, and let $|\{S_{gi}\}|$ and $\{|S_{gi}|\}$ be the number of entries in $\{S_{gi}\}$ and the number of pending vertices in S_{gi}, respectively. Define by $S_{sj}(S_{gi})$ the unique subtree of S_{sj} that has leaves labeled exclusively with species from $|\{S_{gi}\}|$, so that each element of $|\{S_{gi}\}|$ is used i.e., that is, the unique subtree obtained by eliminating from S_{sj} all species that are not present in $|\{S_{gi}\}|$.

Then define similarity measure, σ, between S_{gi} and S_{sj} in the following way:

$\sigma(S_{gi},S_{sj}) = 0$ if $|S_{gi}| \neq |\{S_{gi}\}|$, or S_{sj} (S_{gi}) $\neq S_{gi}$, and

$\sigma(S_{gi},S_{gi}) = |S_{gi}|$

The support of tree clusters by data can be measured using the bootstrap technique described in Felsenstein (1985, Evolution 39:783-791).

In an embodiment of the invention, the human antiquitin gene was identified using phylogenetic analysis. The aldehyde dehydrogenase gene family in humans can be subdivided into at least ten ancient subtrees characterized by different functions of corresponding proteins. These genes probably arose from a series of gene duplications of an ancestral gene which took place before the divergence of a common ancestor of Eukaryotes and Eubacteria.

The aldehyde dehydrogenase gene cluster is highlighted in Figure 6 which shows the original tree of ALDH sequences, the circled area indicating a sequence cluster where bacterial (*Bacillus subtilis*), plant (*Brassica napus*), and nematode (*Caenorhabditis elegans*) ortholog is present, but a human ortholog is not known. A random screening of cDNA libraries showed that a human ortholog, referred to as antiquitin, does exist. Figure 7 shows the same gene tree as in Figure 6 with an additional human protein referred to as antiquitin present in the tree.

In yet another embodiment of the invention, a human ortholog of the murine Max-interacting transcriptional repressor Mad3 was identified through phylogenetic analysis of a gene family. The gene tree was constructed as follows. The protein sequences of known members of the *Mad* gene family were extracted from GenBank database. The extracted sequences were aligned using multiple alignment program CLUSTALW running on Sun SPARC station. Redundant and non-homologous sequences as well as distant homologs from *S. cerevisiae*, *C. elegans*, *D. melanogaster* etc. were removed from the alignment. The refined set of sequences were realigned with CLUSTALW and a gene tree as presented in Figure 18A was computed. To identify a human ortholog of the Mad3 protein, a human dbEST at NCBI was searched with program TBLASTN using mouse Mad3 protein sequences as a query. Two highly homologous ESTs were identified and are presented in Figure 17A. To obtain a complete coding sequence a search was

conducted to obtain overlapping sequences in dbEST. The search for overlapping sequences was performed using the program Iterate with EST Zs77e55.rl (gb/AA278224) as the search query. The search identified a single overlapping sequence. The search for overlapping sequences was performed using program Iterate with EST zs77e55.rl (gb/AA278224) serving as a query. The search returned a single overlapping sequence, namely HUMGS0012279 (dbj/C02407), thus showing that the two EST sequences found during the initial TBLASTIN search belong to the same gene. The complete sequence of the gene was assembled from the two ESTs using commercially available sequence assembly program SeqMan11(DNASTAR Inc., WI). The nucleotide sequence of the human Mad3 gene is presented in Figure 17B. The deduced amino acid sequence of which is presented in Figure 17C. The complete DNA sequence is also shown.

The present invention relates to nucleic acid molecules encoding the human Mad3 protein shown in Figure 17C. The invention also relates to nucleic acid molecules that hybridize to the nucleic acid molecule of Figure 17B under conditions of high stringency and encode a Mad3 protein. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 mg/ml denatured salmon sperm DNA and 5-20 x 10^6 CpM of ^{32}P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.5. SIMULATION AND HYPOTHESIS TESTING

The simulation and hypothesis testing methods of the invention, described in the subsections below, utilize specialized databases of gene/protein structures and interactions for identifying potentially undiscovered members of

multigene families through comparisons of regulatory networks for different species, searching expressed sequence tag (EST) databases, and simulation of regulatory cascades.

5.5.1. GENE DISCOVERY THROUGH ANALYSIS OF REGULATORY NETWORKS

The present invention provides a method for identifying undiscovered genes through comparisons of regulatory networks for different species where functionally similar regulatory systems are conserved. The amount of information available concerning regulatory genes and/or proteins in different organisms and their functional relationships allows one to reconstruct and compare regulatory networks. Since in most cases, the knowledge of all genes involved in almost any particular regulatory system is incomplete, a comparison of homologous networks within the same organism and between different species permits the identification of genes absent in a system under comparison.

The identified genes, being part of a regulatory network, are implicated as potentially contributing to a phenotype of a disease associated with the system under analysis. Using the methods of the present invention these putative disease genes can be cloned, mapped and analyzed for mutations directly, thereby omitting the expensive and time-consuming steps of positional cloning and sequencing of genomic regions. Gene discovery by analysis of regulatory networks is outlined in Figure 8. The analysis is initiated starting with a biological system (*e.g.*, signaling pathway of genes involved in Bcl-2-regulated apoptosis in lymphocytes), a single gene (e.g., Bcl-2) or a gene family (e.g., caspases).

Initially, a specialized database is generated for comparison of regulatory networks between different species. For example, starting with a single candidate gene in a single species, a typical iteration in this process begins with identification of all known proteins and genes that are upstream and downstream with respect to it in regulatory hierarchies and the reconstruction of a network of interacting genes and proteins. Next, for each protein, a set of key domains and motifs is identified and this information is used to search for related proteins in humans and

other species. The identified sequences are compared and for each pair of sequences showing similarity above a certain threshold, a similarity object is generated. A similarity object is generated if two sequences, nucleotide or amino acid, show significant similarity in database searches (p value < 0.001). The object retains the following information: (i) reference to similar substances *i.e.*, genes or proteins; (ii) significance of the similarity, similarity score and percent of identity; and (iii) coordinates of the similarity region within two compared sequences. "Orthology objects" constitute a subset of "similarity objects" which satisfies one additional requirement, *i.e.*, that two similar sequences should be identified as orthologs by the tree-based algorithm described above. In identifying orthologs, if gene A is orthologous to gene B, and gene B is orthologous to gene C, gene A is necessarily orthologous to gene C.

In a specific embodiment of the invention, for each species under analysis, orthologous proteins or genes are identified. In a further embodiment of the invention, small orthologous molecules participating in a regulatory network for two or more species may also be identified. Where proteins, genes, or molecules are orthologs, the action of the protein, gene or molecule between species may be interchangeable. If more than two species are involved in the analysis, subtrees of orthologous substances and subtrees of orthologous actions are identified.

Once orthologous genes, proteins or molecules are identified in two or more species, by forming a reconciled tree, for example, a set of orthologous or paralogous regulatory networks can be analyzed and visualized using graph theory where arcs represent actions and vertices represent substances. Thus, the method of the invention may further comprise the following steps: (i) superimposing the orthologous regulatory networks from two or more species and searching for the actions (arcs) and substances (vertices) in the homologous networks that are represented in some taxa but absent in others; (ii) superimposing paralogous regulatory networks from the same taxa and searching for paralogous genes that are missing in some taxa; and (iii) computing a general regulatory network that summarizes common regulatory sequence relationships known for more than one species.

In a specific embodiment of the invention a set of regulatory networks from different species, relating to the same biological system, apoptosis, for example, can be analyzed and visualized utilizing the following methods: (i) for each species functional information is collected relating to apoptosis; (ii) using the functional information, regulatory networks for each species comprised of interacting proteins and/or the genes involved in apoptosis are generated; (iii) the sequences of the interacting proteins and genes of each of the regulatory network are compared and for sequences showing similarity above a predetermined threshold range; and (iv) distinguishing between orthologs and paralogs using the methods set forth above.

An analysis similar to that performed using subtrees of sequences may be applied to classify protein functions as orthologous or paralogous actions. A "generalized" regulatory network maybe represented as a network wherein a substance as it occurs in a particular species is substituted with a cluster (i.e., subtree) of orthologous substances among species. In the final step of the analysis the clusters within each species are compared to one another, to identify missing genes.

Figure 11 depicts the regulatory relationships among hypothetical proteins (denoted with Arabic numerals) of hypothetical species A and B. As indicated in Figure 11A, an overlay of regulatory data for two species overlaps, but not completely. As indicated, protein 5 is known only for species B while protein 3 is known only for species A. The proteins in different species denoted with the same numeral are considered orthologous. As indicated, the regulatory relationships between a pair of proteins can be of three different kinds. Figure 9B, 9C, and 9D represent Boolean operations, OR, AND, and XOR, as arcs of the two regulatory relationships depicted in Figure 9A, the same operations being applicable to the set of vertices of the two regulatory relationships.

In some instances, orthologous networks in two distantly related taxa may have the same domains but arrangement of the domains between the related taxa may be different. In such a case, a one-to-one correspondence between orthologous proteins in closely related species has to be substituted with a one-to-many relationship among domains comprised within the proteins. For this purpose, a similarity object may be defined operating on pairs of motifs/domains in two proteins, and substitute pairs of

orthologous proteins with pairs of orthologous domains. After this correction, homologous networks are compared as described above.

Figure 10 is a diagram representing a hypothetical example of defining homologous protein networks in two different species using protein motifs, the diagram showing only two hypothetical proteins (lane 2) for species A and three hypothetical proteins (lanes 1, 3, and 4) for species B. Protein 1 in both species has motifs α and β, protein 2 has motifs δ, ϵ, and ζ, and proteins 3 and 4 have motifs δ and ζ, and ϵ, respectively. The motif analysis indicates that proteins 3 and 4 in species B may collectively perform the same function as protein 2 in species A.

5.5.2 GENE DISCOVERY BASED ON PROTEIN MOTIF/DOMAIN SEARCHES

The present invention provides yet another method for identifying genes that are homologous and perform the same or an analogous function in different species. The method of the invention comprises the following steps: (i) creating a database of sequences which comprise a motif or domain composition of a gene of interest using, for example, HMMER software; and (ii) searching additional databases for expressed sequence tags (ESTs) containing the domains and motifs characteristic for the gene of interest with HMMs of domains and motifs identified in step (i). In yet another embodiment of the invention, sequences may be searched which correspond to nucleotide sequences in an EST database or other cDNA databases using a program such as BLAST and retrieving the identified sequences. In an optional step, for each EST identified, sequence databases can be searched for overlapping sequences for the purpose of assembling longer overlapping stretches of DNA. Once identified, the ESTs can be used to isolate full length nucleotide sequences comprising the gene of interest using methods such as those described in Section 5.4, *infra*.

The general flowchart scheme for gene discovery analysis based on motif/domain search is shown in Figure 11. In a specific embodiment of the invention, the method referred to as the "phylogenetic reflection technique"comprises, first, defining the motif or domain composition of a gene of interest involved in a biological system of interest. Second, protein-coding genes from other species,

including for example yeast and/or nematode genes, that bear a significant similarity to the gene of interest or a specified domain of the corresponding protein are collected. Third, the identified genes are in turn subjected to a "domain analysis" to establish protein motifs which might suggest a function of these genes using, for example, HMMER software. Fourth, the selected genes are in turn used for database searches in EST databases (dbEST) and/or a non-redundant (nr) database to identify unknown genes that are potentially orthologous to the selected yeast and nematode genes. Once identified ESTs having different tumor suppressor domains may be linked using multiple PCR primers. Using routine cloning techniques, well known to those of skill in the art, a full length cDNA representing the gene of interest can be obtained.

Once new genes are identified by domain/motif analysis experimental searches may be carried out to isolate complete coding sequences and evaluate their tissue- and disease-specific expression patterns. In parallel their position with respect to regulatory networks can be identified as described below.

In a specific embodiment of the invention, an apoptosis related human gene was identified using the method described above. As a first step *C. elegans* genes containing either POZ or Kelch domains were identified. A Hidden Markov Model was developed using POZ and Kelch sequences from the *Drosophila* Kelch protein and any identified homologs. The resulting Hidden Marker Model was used to search through the collection of *C. elegans* protein sequences. One of the identified *C. elegans* genes contained a POZ domain, death domain, kinase domain and heat repeat. The presence of both a death domain and a kinase domain suggested that the protein functions as a regulatory protein.

A human EST database was searched using the protein sequence of the identified *C. elegans* gene and two sequences were identified (Figure 14A). A gene tree was computed to determine whether the identified human sequences were orthologs of the *C. elegans* gene. As depicted in Figure 14B, the human EST AA481214 appears to be a true ortholog of the *C. elegans* gene. Figure 14C presents the nucleotide sequence of the identified death domain gene. Figure 14D presents the amino acid sequence of the death domain protein.

The present invention encompasses the nucleic acid molecule of Figure 14C, comprising the sequence of EST AA481214 and proteins encoded by said nucleic acid molecule. The invention also relates to nucleic acid molecules capable of hybridizing to such a nucleic acid molecule under conditions of high stringency. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 mg/ml denatured salmon sperm DNA and 5-20 x 10^6 CpM of ^{32}P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.5.3. SIMULATION OF REGULATORY CASCADES

In an embodiment of the invention, an interactive graphical program is utilized for visualizing the scheme of regulatory relationships, "current" states of the substances, and active and inactive actions between pairs of substances. Such a program can be utilized for identification of genes which are associated with a specific disease. Currently, disease associated genes are discovered through positional cloning methods which combine methods of genetics and physical mapping with mutational analysis. The present invention provides a novel method for discovering disease associated genes. For simulating regulatory cascades, it is assumed that the time in a simulated regulatory system advances in discrete "quanta," or periods of time. The "state of substances" of the system for each discrete period of time is computed by: creating a set of substance objects, where a set of interactions between each created substance object is known, an initial state is specified. The time is initially set to zero. All defined actions are observed to confirm that the substances corresponding to the actions (i) exist, and (ii) are in the right initial states. Action is defined by a pair of substances that are in suitable states. The "subject" substance is in the inactive state,

while the "object" substance can be in either active, or inactive, state depending on the action type. For example, the action "dephosphorylation" requires an active phosphatase ("subject" substance) and a phosphorylated substitute protein ("object" substance) in phosphorylated form. If both conditions are satisfied, the action is recorded as in progress. At termination, the substances must change their states as specified by the action. On each following "quantum" of time, the simulation proceeds in the same way while maintaining the "bookkeeping" of the remaining time for each action and the remaining lifespan of each substance. The simulation stops when there are no more active actions available. The program allows editing of the properties of the objects, changing the scale and focus of the visualized simulation, and experimenting with the systems output.

In a specific embodiment of the invention a "knock out" of a gene can be simulated to model the regulatory system that normally includes hypothetical gene A. One of the typical questions related to the gene knock out is how does the knock out affect a biological pathway of interest. A hypothetical example of evaluating the impact of a knock out of hypothetical gene A on the expression of a hypothetical gene B is shown in Figure 12. The answer to such a question could be "gene B will be inhibited" or "gene B will be induced" or "no effect".

In the practice of the present invention, a simple algorithm involving multiplication of gene interaction "signs" along the shortest pathway between the genes can be used to determine the outcome. The algorithm involves the following steps: (i) identification of the shortest non-oriented pathway connecting genes A and B involved in a pathway of interest; (ii) assigning sign "-" to gene A since it is knocked out and taking this sign as the initial sign value; (iii) moving along the shortest pathway between genes A and B, multiplying the current value of the sign with the sign of the next arc, where "-" stands for inhibition, "+" stands for induction or activation, and "0" stands for the lack of interaction between two proteins in the specified direction; (iv) determining if the final result of multiplication is "0", if so eliminating the zero arc and trying to find the shortest oriented bypass pathway between A and B in the remaining network; otherwise stop. The final value of the sign at the moment of arriving at vertex B would indicate the most likely effect of the

knock out of gene A which can be any one of the following: inhibition of gene B, induction/activation of gene B, or none. In addition to the "electronic knock out", an "electronic knock in" of a particular gene can be simulated. In such a computer simulation, the artificial addition of a gene and its effect on a regulatory system may be analyzed.

5.6. IDENTIFICATION AND ISOLATION OF NOVEL GENES

The present invention relates to identification of novel genes, i.e., missing orthologs or paralogs, and the isolation of nucleic acid molecules encoding novel genes. In a specific embodiment, a nucleic acid molecule encoding a missing ortholog or paralog can be isolated using procedures well known to those skilled in the art (See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York Glover, D.M. (ed.), 1985, DNA Cloning: A Practical Approach MRL Press, Ltd., Oxford, U.K. Vol. I, II.).

For example, genomic and/or cDNA libraries may be screened with labeled DNA fragments derived from a known ortholog or paralog from a specific species and hybridized to the genomic or cDNA libraries generated from a different species. For cross species hybridization, low stringency conditions are preferred. For same species hybridization, moderately stringent conditions are preferred. Any eukaryotic cell potentially can serve as the nucleic acid source for the molecular cloning of the gene of interest. The DNA may be obtained by standard procedures known in the art from cloned DNA (e.g., a DNA "library"), by cDNA cloning, or by the cloning of genomic DNA, or fragments thereof, purified from the desired cell.

By way of example and not limitation, procedures using conditions of low stringency are as follows (see also Shilo and Weinberg, 1981, Proc. Natl. Acad. Sci. USA 78:6789-6792; and Sambrook et al. 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring harbor, New York): Filters containing DNA are pretreated for 6 h at 40°C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 mg/ml denatured salmon sperm DNA. Hybridizations are

carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate, and 5-20 X 10^6 cpm ^{32}P-labeled probe is used. Filters are incubated in hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55°C in a solution containing 2X SSC, 25 mM Tris-HC1 (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Filters are blotted dry and exposed for autoradiography. If necessary, filters are washed for a third time at 65-68°C and reexposed to film. Other conditions of low stringency which may be used are well known in the art (*e.g.*, as employed for cross species hybridizations).

In another specific embodiment, a nucleic acid which is hybridizable to a nucleic acid under conditions of moderate stringency is provided. For example, but not by way of limitation, procedures using such conditions of moderate stringency are as follows: filters containing DNA are pretreated for 6 h at 55°C in a solution containing 6X SSC, 5X Denhart's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution and 5-20 X 10^6 CpM ^{32}P- labeled probe is used. Filters are incubated in the hybridization mixture for 18-20 h at 55°C, and then washed twice for 30 minutes at 60°C in a solution containing 1X SSC and 0.1% SDS. Filters are blotted dry and exposed for autoradiography. Other conditions of moderate stringency which may be used are well-known in the art. Washing of filters is done at 37°C for 1 h in a solution containing 2X SSC, 0.1% SDS.

For expression cloning (a technique commonly used in the art), an expression library is constructed. For example, mRNA is isolated from the cell type of interest, cDNA is made and ligated into an expression vector (*e.g.*, a bacteriophage derivative) such that it is capable of being expressed by a host cell (*e.g.*, a bacterium) into which it is then introduced. Various screening assays can then be used to select for the expressed gene product of interest based on the physical, chemical, or immunological properties of its expressed product. Such properties can be deduced from the properties of the corresponding orthologs from other species.

In another embodiment, polymerase chain reaction (PCR) can be used to amplify the desired sequence from a genomic or cDNA library. To isolate orthologous or paralogous genes from other species, one synthesizes several different degenerate primers, for use in PCR reactions. In a preferred aspect, the oligonucleotide primers represent at least part of the gene comprising known ortholog or paralog sequences of different species. It is also possible to vary the stringency of hybridization conditions used in priming the PCR reactions, to allow for greater or lesser degrees of nucleotide sequence similarity between the known nucleotide sequences and the nucleic acid homolog being isolated.

Synthetic oligonucleotides may be utilized as primers to amplify by PCR sequences from a source (RNA or DNA), preferably a cDNA library, of potential interest. PCR can be carried out, *e.g.*, by use of a Perkin-Elmer Cetus thermal cycler and a thermostable polymerase, *e.g.*, Amplitaq (Perkin-Elmer). The nucleic acids being amplified can include mRNA or cDNA or genomic DNA from any eukaryotic species. After successful amplification of a segment of a the gene of interest, that segment may be molecularly cloned and sequenced, and utilized as a probe to isolate a complete cDNA or genomic clone.

Once identified and isolated the gene of interest can then be inserted into an appropriate cloning vector for amplification and/or expression in a host. A large number of vector-host systems known in the art may be used. Possible vectors include, but are not limited to, plasmids and modified viruses, but the vector system must be compatible with the host cell used. Such vectors include, but are not limited to, bacteriophages such as lambda derivatives, or plasmids such as pBR322 or pUC plasmid derivatives or the Bluescript vector (Stratagene). The insertion into a cloning vector can, for example, be accomplished by ligating the DNA fragment into a cloning vector which has complementary cohesive termini.

6. EXAMPLE: USE OF SPECIALIZED DATABASES FOR IDENTIFICATION OF NOVEL GENES

To test the method of using databases for gene discovery, protein sequence and domain/motif databases specific to two overlapping functional

groupings of proteins: (i) proteins known to be tumor suppressors, and (ii) proteins implicated in apoptosis in animals were developed.

6.1 APOPTOSIS GENE DISCOVERY METHOD

Identification of a putative apoptosis-related human gene began with an identification of all genes in *C. elegans* that contained either a POZ or kelch domain. A subset of these genes is shown in Figure 13. Hidden Markov Models (HMM) for the POZ and Kelch domains were built as follows. Starting with POZ and kelch sequences from the *Drosophilia* kelch protein (gi|577275) homologs were identified in other protein sequences using the BLASTP program. The resulting sequences showing significant similarity (e-value less than 0.001) were aligned using CLUSTALW program and the alignments were used to build Hidden Markov Models with HMMER-2 package (Krogh et al., 1995, :http://hmmer.wustl.edu/). A computer printout listing of HMM models of tumor suppressors appears as a Microfiche H to the present specification. (See, http://hmmer.wustl.edu; Chapter 2, which is incorporated by reference herein in its entirety, for a detailed description of HMM models)

The resulting models were used to search through a database collection of *C.elegans* protein sequences. The domain structures of proteins having either a POZ or kelch domain were identified using existing collections of protein domains (e.g., see http://blocks.fhcrc.org/blocks/blocks release.html, http://coot.embl-heidelberg.de/SMART/, http://www.motif.genome.ad.jp/). One of the unannotated protein-coding genes of *C. elegans* (corresponding protein accession number gi|1132541, see Figure 11) appeared to include a POZ domain, death domain, kinase domain, and heat repeat. A death domain is characteristic for the apoptosis system and a kinase domain indicates that the protein is likely to participate in phosphorylation of other proteins. The presence of these particular domains suggests that this protein is serving as a regulatory protein.

Using the protein sequence of gi|1132541, the database of human EST sequences was searched and a number of partial human cDNA sequences representing potential human orthologs or paralogs of the *C.elegans* gi|1132541 were identified.

The two closest human sequences, AA481214 and W51957, are depicted in Figure 14A. To determine whether the identified human sequences were orthologs or paralogs to the gi|1132541 gene of *C. elegans*, a gene tree (Saito and Nei, 1997, Molecular Biol. Evol. 4:406-425) was computed. The gene tree was generated using homologous genes identified with a BLASTP search against NCBI non-redundant database, using the human EST AA481214 sequence as a query. The resulting tree indicates that the identified human EST AA481214 represents a true ortholog of the *C.elegans* gene gi|1132541 (Figure 14B). The nucleotide sequence of the death domain protein is shown in Figure 14C, as well as the deduced amino acid sequence presented in Figure 14D.

6.1.2 APOPTOSIS GENE DISCOVERY METHOD

As a first step in identifying a novel gene involved in apoptosis, a comprehensive set of articles describing the system of apoptosis/programmed cell death in different species was compiled using the keyword "apoptosis". By analyzing the articles, information on regulatory pathways characterizing this system in different species, *i.e.*, *C. elegans*, mouse, fruit fly, chicken, and human, was extracted. The regulatory information was stored as a collection of schemes produced in PowerPoint (Microsoft). Figure 4 shows a set of keywords defining proteins involved in apoptosis pathways. The keywords were used to generate a specialized sequence database, referred to as Apoptosis3, utilizing the PsiRetriever program for extraction of proteins from the all-inclusive non-redundant GenBank database (NCBI). Using program PsiRetriever, sequences from the non-redundant (NCBI) database of protein sequences, were retrieved and stored as a FASTA file. The FASTA file was then converted into binary blast database using program FORMATDB from the BLAST suit of programs.

Genomic and cDNA sequences located in the region of human chromosome 13q were compared with the Apoptosis3 database using BLASTALL program from BLAST program complex. This region of the human genome is associated with Chronic Lymphocytic Leukemia (CLL). The comparison revealed significant similarity between a CLL region open reading frame and the mouse RPT1

protein (sp|P15533|RPT1) (Figure 13). Analysis of regulatory functions of RPT1 in the mouse reveals that this gene functions as a repressor of the interleukin 2 receptor (IL-2R) gene. When the RPT1 gene is knocked out, the regulatory effect is manifested as a block of the apoptotic pathway in T lymphocytes resulting in an accumulation of T lymphocytes in blood. This result is consistent with aberrations observed in CLL, namely abnormal accumulation of B-cells in the blood (Trentin L. et al., 1997, Leuk. Lymphoma 27:35-42) and mutations in the human RPT1 gene play a role in development of CLL.

6.1.3 EXAMPLE: A DISCOVERY OF A HUMAN ORTHOLOG OF THE MURINE MAX-INTERACTING TRANSCRIPTIONAL REPRESSOR

The family of *Myc* proto-oncogenes encodes a set of transcription factors implicated in regulation of cell proliferation, differentiation, transformation and apoptosis. C-*Myc* null mutations result in retarded growth and development of mouse embryos and are lethal by 9-10 day of gestation. In contrast, overexpression of *Myc* genes inhibits cell differentiation and leads to neoplastic transformation. Moreover, deregulation of *Myc* expression by retroviral transduction, chromosomal translocation or gene amplification is linked to a broad range of naturally occurring tumors in humans and other species.

Another protein, called *Max*, is an obligatory heterodimeric partner for *Myc* proteins in mediating their function as activators of transcription during cell cycle progression, neoplastic transformation and programmed cell death (apoptosis). In order to make an active transcription factor the *Myc* proteins must form heterodimers with *Max* protein. This interaction with *Max* protein is necessary for specific binding of *Myc* with CACGTG box (or related E-boxes) on DNA and for activation of promoters located proximal to the binding sites.

Besides the *Myc* family of transcription factors, the *Max* protein forms complexes with another family of so-called *MAD* proteins: *Mxi1*, *MAD1*, *MAD3* and *MAD4*. Whereas *Myc*:*Max* complexes activate transcription, *MAD*:*Max* complexes work in an opposite way repressing the transcription through the same E-box binding

sites and apparently antagonize *Myc*-mediated activation of the same set of target genes.

During tissue development a shift from *Myc*:*Max* to *MAD*:*Max* complexes occurs coincidentally with the switch from cell proliferation to differentiation. The switch in heterocomplexes is thought to reflect a switch from activation to repression of common genes leading to cessation of proliferation, exiting the cell cycle and the beginning of cell differentiation. In differentiating neurons, primary keratinocytes, myeloid cell lines and probably other tissues the expression of different *MAD*:*Max* complexes appear in sequential order during the transition from cell proliferation to differentiation. The *MAD3* expression appears first and it is restricted to proliferating cells prior to differentiation where it is co-expressed with two different member of *Myc* family, c-*Myc* or N-*Myc*. *Mxi1* transcripts are detected in proliferating and differentiating cells whereas *MAD1* and *MAD4* were confined to post-mitotic cells. Because *Myc* expression is not always downregulated in post-mitotic cells, co-expression of *Myc* and *MAD* genes may result in competition for *Max* heterodimers thus providing promoting or inhibitory effect on cell proliferation.

The gene expression patterns, along with ability of Mad proteins to suppress *Myc*-dependent transformation, are consistent with a potential function of Mad genes as tumor suppressors. This view is supported by the fact that allelic loss and mutations were detected at the *Mxi1* locus in prostate cancers (Eagle et al., 1995 Nat Genet 9:249-55). Cloning of the murine proteins *Mad3* and *Mad4* as well as their relation to *Max* signaling network was described by Hurlin (Hurlin PJ, et al., 1995, EMBO J. 14:5646-59) and Queva (Queva et al. 1998 Oncogene 16:967-977). Human orthologs of *Mad4*, *Mad1* and *Mxi1* are known.

In this example, the discovery of an unknown human ortholog of *Mad3* protein found "*in silico*," by means of phylogenetic analysis of known mouse and human members of the *Mad* gene family and database searches is described. Since the function of murine *Mad3* as a *Max*-interacting transcriptional repressor of *Myc*-induced neoplastic transformation is well described, we can assign the same function to its human ortholog.

The gene tree shown in the Figure 20 was constructed in the following way. The protein sequences of known members of *Mad* gene family were extracted from GenBank database using NCBI Entrez keyword searches. The extracted sequences were aligned using multiple alignment program Clustalw running on Sun SPARC station. The quality of the multiple alignment was checked using program HitViewer Iterate (A. Rzhetsky, available upon request) and the redundant, non-homologous sequences as well as distant homologs from *S. cerevisiae, C. elegans, D. melanogaster* etc. were removed from the alignment. The refined set of sequences was realigned with Clustalw and a gene tree as presented in Figure 15A was computed from the alignment using program NJBOOT (http://genome6.cpmc.columbia.edu // andrey) running on Sun SPARC station and viewed with program TreeView (http://genome6.cpmc.columbia.edu // andrey).

The tree presented in Fig.19A clearly shows the relationships between three known mouse genes and their two human homologs. Attempts to find a missing human ortholog of the mouse *Mad3* gene in protein non-redundant database at NCBI using BLAST search did not identify any human homologs other than sequences that were already present on the tree, confirming the absence of a known human ortholog for Mad3 protein in the database.

In order to identify a human ortholog of the Mad3 protein, a human dbEST at NCBI was searched with program TBLASTN using Mad3 protein sequence as a query. Two EST were identified and are shown in Figure 17A.

Due to the nature of dbEST database this search produced only partial sequences of potential candidate genes. To obtain complete coding sequences (complete cds) of the genes, a search was conducted to obtain overlapping sequences in dbEST. The search for overlapping sequences was performed using the program Iterate with EST zs77e55.r1 (gb|AA278224) serving as a query. The search returned a single overlapping sequence, namely HUMGS0012279 (dbj|C02407), thus indicating that the two EST sequences found during the initial TBLASTN search belong to the same gene.

The complete sequence of the gene was assembled from the two ESTs using commercially available sequence assembly program SeqManII (DNASTAR Inc.,

WI). The nucleotide sequence of the human *Mad3* gene is presented in Figure 17B. The deduced amino acid sequence of the gene is presented in Figure 17C. The translated sequence consists of 206 amino acid residues 81% of which are identical to mouse Mad3 protein. The alignment of human and mouse Mad3 proteins shown below was made using BLAST server at NCBI and is presented in Figure 17C.

Multiple alignment of the new sequence with sequences of known Mad proteins was made using Clustalw and viewed with the HitViewer. A gene tree was computed from this alignment using NJBOOT. Multiple alignment of the new sequence with sequences of known Mad proteins (Figure 17C) along with its position on gene tree (Figure 18B) shows that this new human gene found by the approach described above belongs to the family of Mad proteins and is the ortholog of mouse Mad3.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the contents of which are hereby incorporated by reference in their entireties.

CLAIMS

1. A method for identifying a novel nucleic acid molecule encoding a protein of interest comprising:

(i) selecting a specific protein from a first species involved in a regulatory network of interest;

(ii) identifying known proteins that act upstream and downstream in the regulatory network of interest with respect to the specific protein selected;

(iii) constructing the regulatory network of interest from the proteins identified in step (ii);

(iv) for each identified protein, select a domain or motif and search by homology for related proteins in a second species, wherein a related protein is defined as a protein having a homologous domain or motif;

(v) producing a regulatory network for the second species, wherein said regulatory network incorporates the identified related proteins;

(vi) comparing the regulatory network from the first species to the regulatory network of said second species;

(v) identifying a protein present in a regulatory network for one species but absent in the regulatory network of the other species; and

(vi) isolating a nucleic acid molecule encoding the protein identified in step (v) in the species in which it is missing.

2. The method of Claim 1 wherein the nucleic acid molecule encodes human protein.

3. The method of claim 1 wherein the related proteins are orthologs.

4. The method of claim 1 wherein the regulatory pathway is involved in apoptosis.

5. The method of claim 1 wherein the specific protein from the first species is involved in tumor suppression.

6. A method for identifying the affect of a gene knockout on a regulatory pathway comprising the following steps:

(i) identification of the shortest non-oriented pathway connecting two gene products;

(ii) assigning an initial sign value of "-" to the knockout since the knockout gene product is inactive;

(iii) moving along the shortest pathway between the two gene products multiplying the sign with the sign of the next gene product in the pathway, wherein "-" stands for inhibition, "+" stands for induction or activation, and "0" stands for the lack of interaction between two proteins in the specified direction; and

(iv) determining the final sign at the end of the pathway, wherein "-" indicates inhibition and "+" indicates induction or activation of the pathway.

7. A method for identifying a novel nucleic acid molecule encoding a protein of interest comprising:

(i) selecting a gene of interest and searching a database for homologous sequences;

(ii) aligning the homologous sequences identified in step (*i*);

(iii) constructing a gene tree using the sequence alignment;

(iv) constructing a species tree;

(v) imputing the species tree and gene tree into an algorithm which integrates the species tree and the gene tree into a reconciled tree; and

(vi) identifying orthologous genes present in one species but missing in another.

8. The method of claim 7 wherein the following algorithm is used to integrate the species tree and the gene tree into a reconciled tree:

(i) computing the similarity $\sigma(S_{gi},S_{sj})$ for each pair of interior nodes from trees T_g and T_s,

(ii) finding the maximum $\sigma(S_{gi},S_{sj})$;

(iii) saving S_{gi} as a new cluster of orthologs, save $\{S_{gi}\}$ - $\{S_{sj}\}$ as a set of species that are likely to have gene of this kind (or lost it in evolution);

(iv) eliminating S_{gi} from T_g; $T_g := T_g \backslash S_{gi}$;

(v) repeating step (ii)-(iv) until T_g is non-empty.

9. A method for identifying a novel gene comprising the following steps:

(i) defining a motif or domain composition of a gene of interest;

(ii) searching for sequences which correspond to nucleotide sequences in an expression sequence tag database or other cDNA databases using a program such as BLAST and retrieving the identified sequences;

(iii) searching additional databases for expressed sequence tags containing the domains and motifs characteristic for the gene of interest with Hidden Markov Model of domains and motifs identified in step (i);

(iv) identifying nucleotide sequences comprising the gene of interest.

10. The method of claim 9 further comprising using each identified expression sequence tag to search sequence databases for overlapping sequences for the purpose of assembling longer overlapping stretches of DNA.

11. A method for extracting information on interactions between biological entities from natural-language text data, comprising:

(i) parsing the text data to determine the grammatical structure of the text data ;and

(ii) regularizing the parsed text data to form structured word terms.

12. The method according to claim 11, further comprising preprocessing the data prior to parsing, with preprocessing comprising the step of identifying biological entities.

13. The method according to claim 11, further comprising referring to an additional parameter which is indicative of the degree to which subphrase parsing is to be carried out.

14. The method according to claim 11, wherein said parsing step further comprises segmenting the text data by sentences.

15. The method according to claim 11, wherein said parsing step further comprises:

segmenting the text data by sentences; and

segmenting each of the sentences at identified words or phrases.

16. The method according to claim 11, wherein said parsing step further comprises:

segmenting the text data by sentences; and

segmenting each of the sentences at a prefix.

17. The method according to claim 11, wherein said parsing step further comprises skipping undefined words.

18. The method according to claim 11, wherein said parsing step further comprises:

identifying one or more binary actions and their relationships; and

identifying one or more arguments associated with the actions.

19. The method according to claim 11, further comprising performing error recovery when parsing of the text data is unsuccessful.

20. The method according to claim 19, wherein said error recovery step comprises:

segmenting the text data; and

analyzing the segmented text data to achieve at least a partial parsing of the unsuccessfully parsed text data.

21. The method according to claim 11, wherein said tagging step comprises providing the structured data component in a Standard Generalized Markup Language (SGML) compatible format.

22. A computer system for extracting information on biological entities from natural-language text data, comprising:

(i) means for parsing the natural-language text data; and

(ii) means for regularizing the parsed text data to form structured word terms.

23. The system according to claim 22, further comprising means for preprocessing the data prior to parsing, with the preprocessing means comprising identifying biological entities.

24. The system according to claim 22, further comprising means for referring to an additional parameter which is indicative of the degree to which subphrase parsing is to be carried out.

25. The system according to claim 22, wherein said parsing means further comprises means for segmenting the text data by sentences.

26. The system according to claim 22, wherein said parsing means further comprises:

means for segmenting the text data by sentences; and

means for segmenting each of the sentences at identified words or phrases.

27. The system according to claim 22, wherein said parsing means further comprises:

means for segmenting the text data by sentences; and

means for segmenting each of the sentences at a prefix.

28. The system according to claim 22, wherein said parsing means further comprises means for skipping undefined words.

29. The system according to claim 22, wherein said parsing means further comprises:

means for identifying one or more binary actions and their relationships; and

means for identifying one or more arguments associated with the actions.

30. The system according to claim 22, further comprising means for performing error recovery when parsing of the text data is unsuccessful.

31. The system according to claim 22, wherein said error recovery means comprises:

means for segmenting the text data; and

means for analyzing the segmented text data to achieve at least a partial parsing of the unsuccessfully parsed text data.

32. The system according to claim 22, wherein said tagging means comprises means for providing the structured data component in a Standard Generalized Markup Language (SGML) compatible format.

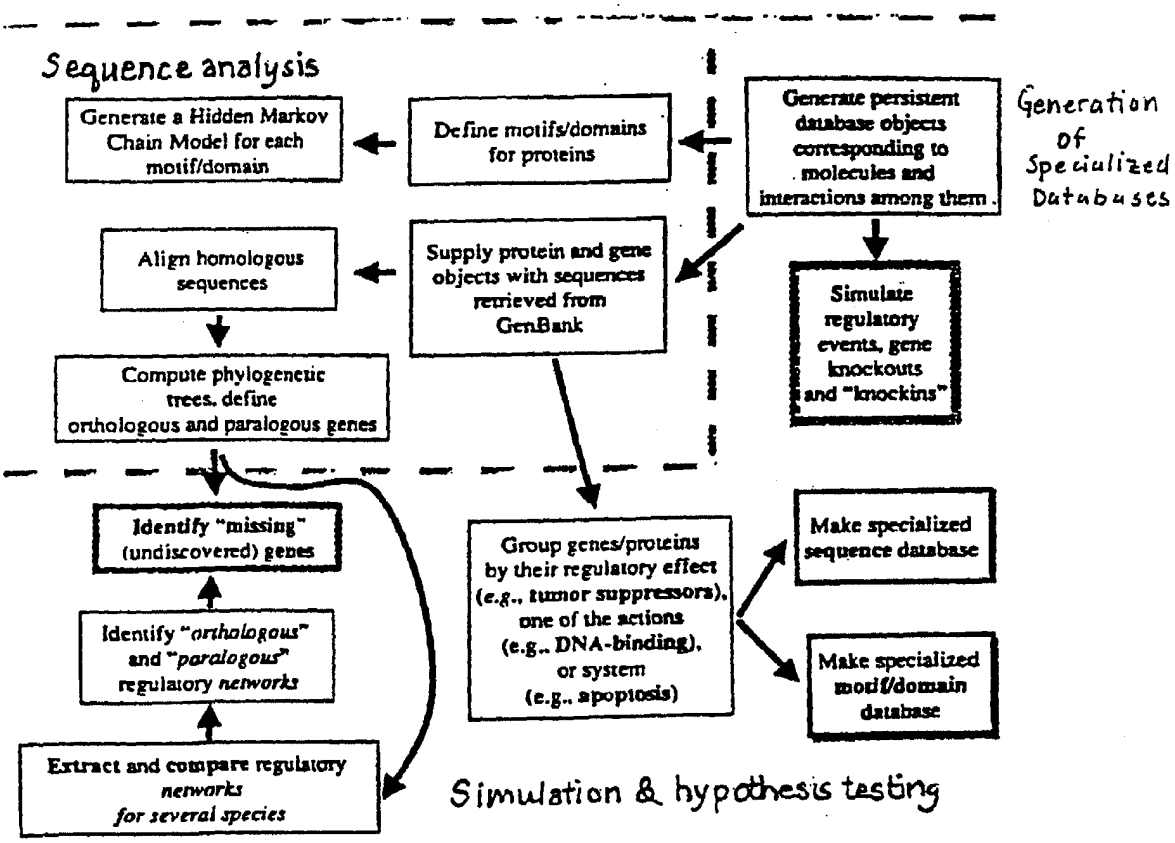

Sequence analysis
Generate a Hidden Markov Chain Model for each motif/domain
Define motifs/domains for proteins
Generate persistent database objects corresponding to molecules and interactions among them
Generation of Specialized Databases
Align homologous sequences
Supply protein and gene objects with sequences retrieved from GenBank
Simulate regulatory events, gene knockouts and "knockins"
Compute phylogenetic trees, define orthologous and paralogous genes
Identify "missing" (undiscovered) genes
Group genes/proteins by their regulatory effect (e.g., tumor suppressors), one of the actions (e.g., DNA-binding), or system (e.g., apoptosis)
Make specialized sequence database
Identify "orthologous" and "paralogous" regulatory networks
Make specialized motif/domain database
Extract and compare regulatory networks for several species
Simulation & hypothesis testing

FIGURE 1

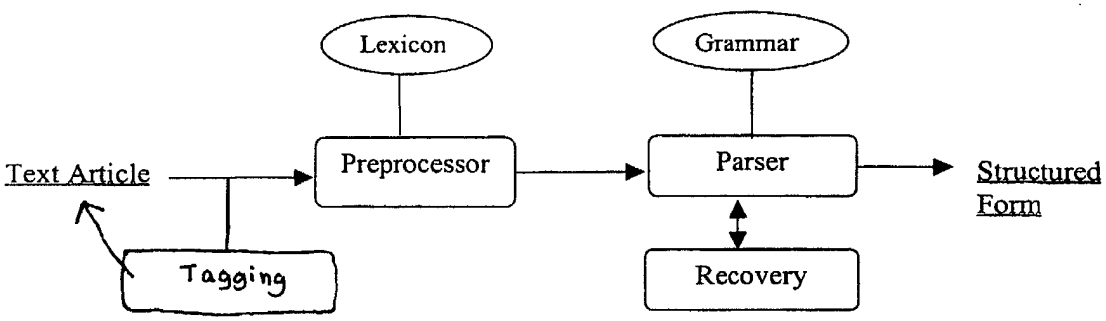

Lexicon
Grammar
Text Article
Preprocessor
Parser
Structured Form
Tagging
Recovery

Figure 2

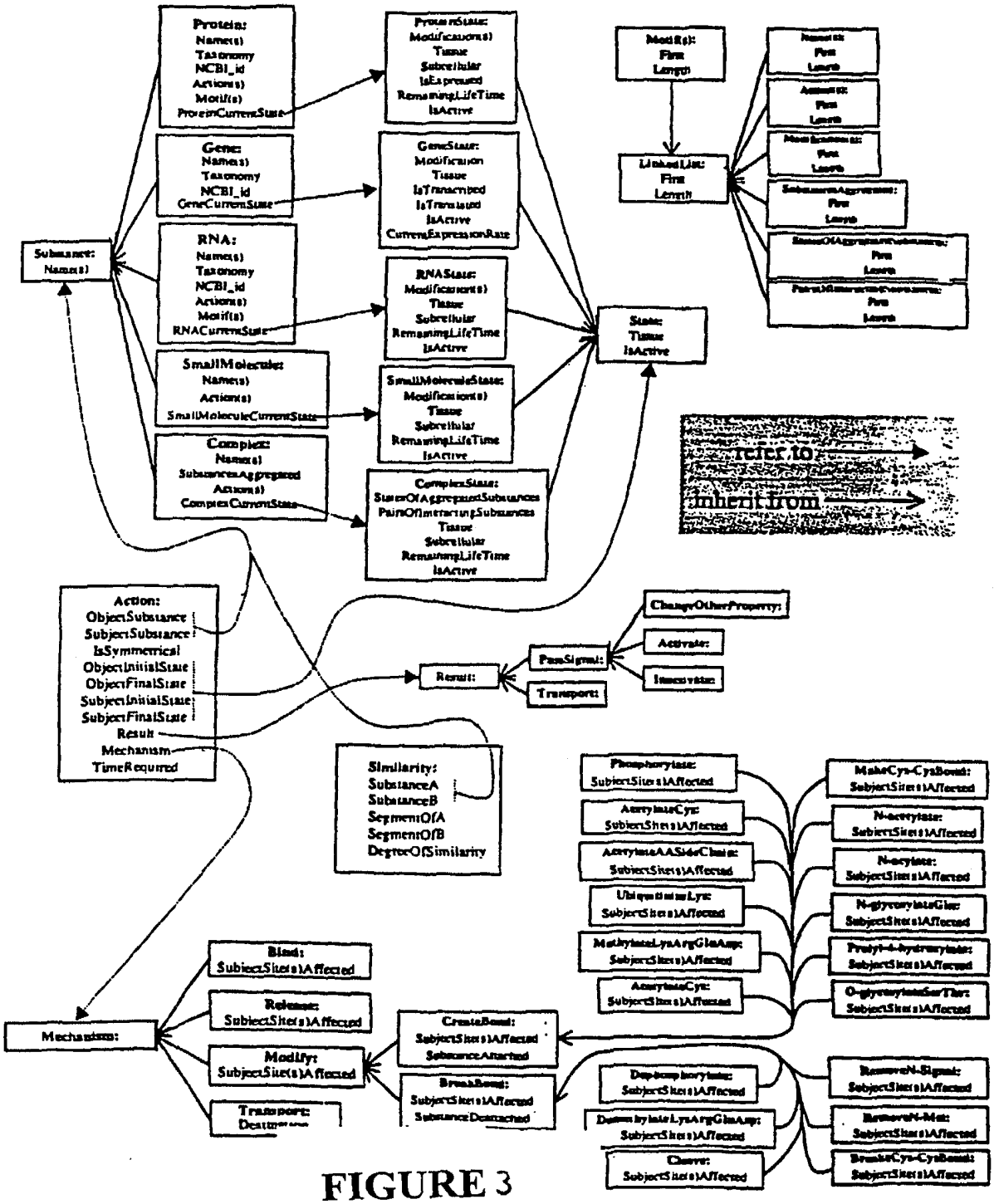
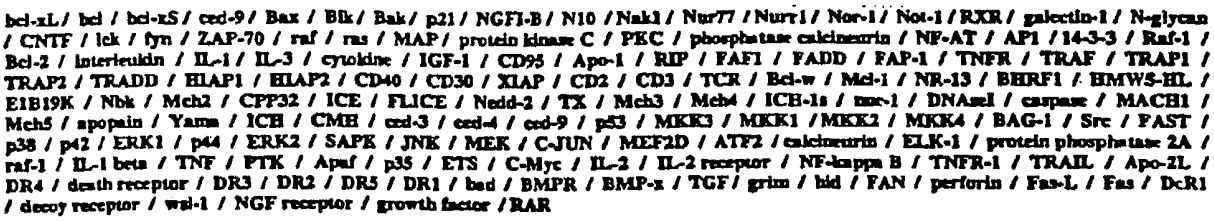

Protein:
Name(s)
Taxonomy
NCBI_id
Action(s)
Motif(s)
ProteinCurrentState
Gene:
Name(s)
Taxonomy
NCBI_id
GeneCurrentState
RNA:
Name(s)
Taxonomy
NCBI_id
Action(s)
Motif(s)
RNACurrentState
SmallMolecule:
Name(s)
Action(s)
SmallMoleculeCurrentState
Complex:
Name(s)
SubstancesAggregated
Action(s)
ComplexCurrentState
Substance:
Name(s)
ProteinState:
Modification(s)
Tissue
Subcellular
IsExpressed
RemainingLifeTime
IsActive
GeneState:
Modification
Tissue
IsTranscribed
IsTranslated
IsActive
CurrentExpressionRate
RNAState:
Modification(s)
Tissue
Subcellular
RemainingLifeTime
IsActive
SmallMoleculeState:
Modification(s)
Tissue
Subcellular
RemainingLifeTime
IsActive
ComplexState:
StatesOfAggregatedSubstances
PairsOfInteractingSubstances
Tissue
Subcellular
RemainingLifeTime
IsActive
Motif(s):
Firm
Length
LinkedList:
Firm
Length
State:
Tissue
IsActive
refer to
inherit from
Action:
ObjectSubstance
SubjectSubstance
IsSymmetrical
ObjectInitialState
ObjectFinalState
SubjectInitialState
SubjectFinalState
Result
Mechanism
TimeRequired
Result:
PassSignal:
ChangeOtherProperty:
Activate:
Inactivate:
Transport:
Similarity:
SubstanceA
SubstanceB
SegmentOfA
SegmentOfB
DegreeOfSimilarity
Mechanism:
Bind:
SubjectSite(s)Affected
Release:
SubjectSite(s)Affected
Modify:
SubjectSite(s)Affected
Transport:
CreateBond:
SubjectSite(s)Affected
SubstanceAttached
BreakBond:
SubjectSite(s)Affected
SubstanceDetached
Phosphorylate:
SubjectSite(s)Affected
AcetylateCys:
SubjectSite(s)Affected
AcetylateAASideChain:
SubjectSite(s)Affected
UbiquitinateLys:
SubjectSite(s)Affected
MethylateLysArgGlnAsp:
SubjectSite(s)Affected
AcetylateCys:
SubjectSite(s)Affected
MakeCys-CysBond:
SubjectSite(s)Affected
N-acetylate:
SubjectSite(s)Affected
N-acylate:
SubjectSite(s)Affected
N-glycosylateGln:
SubjectSite(s)Affected
Prolyl-4-hydroxylate:
SubjectSite(s)Affected
O-glycosylateSerThr:
SubjectSite(s)Affected
Dephosphorylate:
SubjectSite(s)Affected
DemethylateLysArgGlnAsp:
SubjectSite(s)Affected
Cleave:
SubjectSite(s)Affected
RemoveN-Signal:
SubjectSite(s)Affected
RemoveN-Met:
SubjectSite(s)Affected
BreakCys-CysBond:
SubjectSite(s)Affected

FIGURE 3

FIGURE 4


bcl-xL / bcl / bcl-xS / ced-9 / Bax / Blk / Bak / p21 / NGFI-B / N10 / Nak1 / Nur77 / Nurr1 / Nor-1 / Not-1 / RXR / galectin-1 / N-glycan / CNTF / lck / fyn / ZAP-70 / raf / ras / MAP / protein kinase C / PKC / phosphatase calcineurin / NF-AT / AP1 / 14-3-3 / Raf-1 / Bcl-2 / interleukin / IL-1 / IL-3 / cytokine / IGF-1 / CD95 / Apo-1 / RIP / FAF1 / FADD / FAP-1 / TNFR / TRAF / TRAP1 / TRAP2 / TRADD / HIAP1 / HIAP2 / CD40 / CD30 / XIAP / CD2 / CD3 / TCR / Bcl-w / Mcl-1 / NR-13 / BHRF1 / BIMWS-HL / E1B19K / Nbk / Mch2 / CPP32 / ICE / FLICE / Nedd-2 / TX / Mch3 / Mch4 / ICH-1s / nuc-1 / DNAseI / caspase / MACH1 / Mch5 / apopain / Yama / ICH / CMH / ced-3 / ced-4 / ced-9 / p53 / MKK3 / MKK1 / MKK2 / MKK4 / BAG-1 / Src / FAST / p38 / p42 / ERK1 / p44 / ERK2 / SAPK / JNK / MEK / C-JUN / MEF2D / ATF2 / calcineurin / ELK-1 / protein phosphatase 2A / raf-1 / IL-1 beta / TNF / PTK / Apaf / p35 / ETS / C-Myc / IL-2 / IL-2 receptor / NF-kappa B / TNFR-1 / TRAIL / Apo-2L / DR4 / death receptor / DR3 / DR2 / DR5 / DR1 / bad / BMPR / BMP-x / TGF / grim / bid / FAN / perforin / Fas-L / Fas / DcR1 / decoy receptor / wsl-1 / NGF receptor / growth factor / RAR

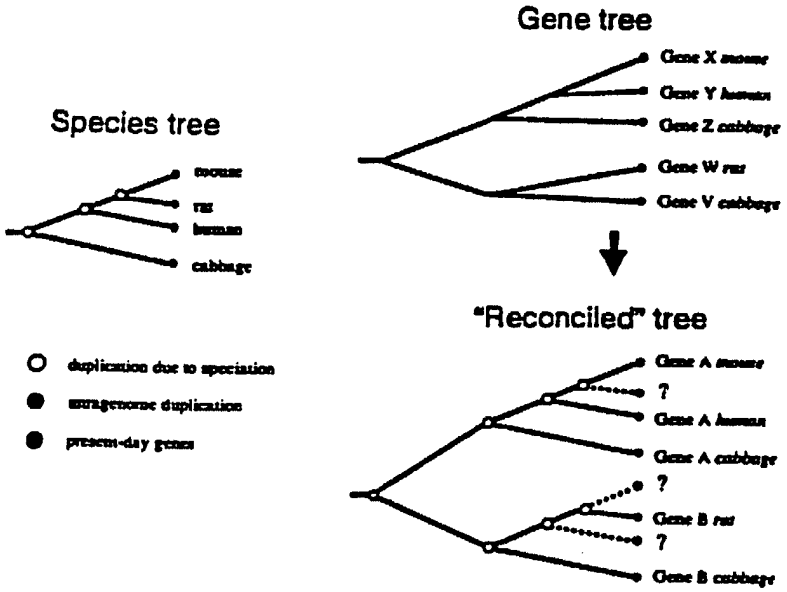

Species tree
mouse
rat
human
cabbage
duplication due to speciation
intragenome duplication
present-day genes
Gene tree
Gene X mouse
Gene Y human
Gene Z cabbage
Gene W rat
Gene V cabbage
"Reconciled" tree
Gene A mouse
?
Gene A human
Gene A cabbage
?
Gene B rat
?
Gene B cabbage

FIGURE 5

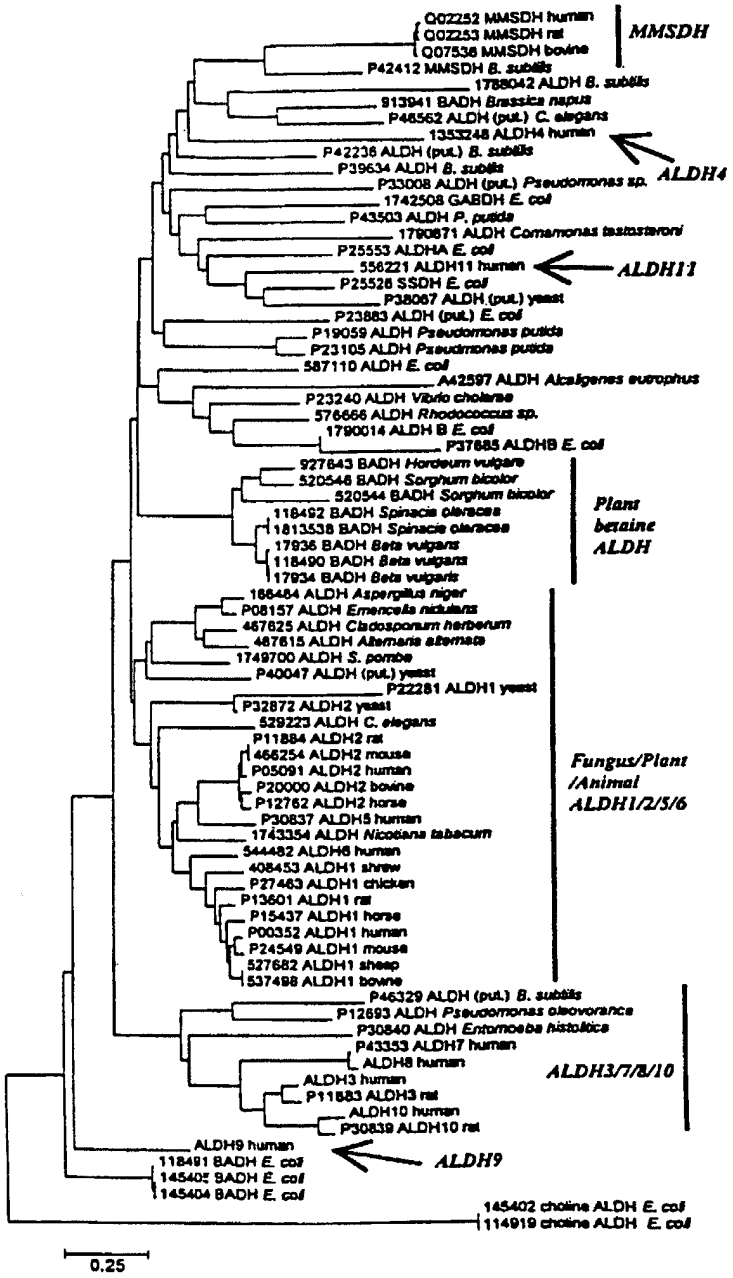

Q02252 MMSDH human
Q02253 MMSDH rat
Q07536 MMSDH bovine
MMSDH
P42412 MMSDH B. subtilis
1788042 ALDH B. subtilis
913941 BADH Brassica napus
P46562 ALDH (put.) C. elegans
1353248 ALDH4 human
P42238 ALDH (put.) B. subtilis
P39634 ALDH B. subtilis
P33008 ALDH (put.) Pseudomonas sp.
ALDH4
1742508 GABDH E. coli
P43503 ALDH P. putida
1790871 ALDH Comamonas testosteroni
P25553 ALDHA E. coli
556221 ALDH11 human
ALDH11
P25526 SSDH E. coli
P38067 ALDH (put.) yeast
P23883 ALDH (put.) E. coli
P19059 ALDH Pseudomonas putida
P23105 ALDH Pseudomonas putida
587110 ALDH E. coli
A42597 ALDH Alcaligenes eutrophus
P23240 ALDH Vibrio cholerae
576666 ALDH Rhodococcus sp.
1790014 ALDH B E. coli
P37685 ALDHB E. coli
927843 BADH Hordeum vulgare
520546 BADH Sorghum bicolor
520544 BADH Sorghum bicolor
Plant betaine ALDH
118492 BADH Spinacia oleracea
1813538 BADH Spinacia oleracea
17936 BADH Beta vulgaris
118490 BADH Beta vulgaris
17934 BADH Beta vulgaris
166484 ALDH Aspergillus niger
P08157 ALDH Emericella nidulans
467825 ALDH Cladosporium herbarum
467615 ALDH Alternaria alternata
1749700 ALDH S. pombe
P40047 ALDH (put.) yeast
P22281 ALDH1 yeast
P32872 ALDH2 yeast
529223 ALDH C. elegans
P11884 ALDH2 rat
466254 ALDH2 mouse
P05091 ALDH2 human
P20000 ALDH2 bovine
P12762 ALDH2 horse
Fungus/Plant /Animal ALDH1/2/5/6
P30837 ALDH5 human
1743354 ALDH Nicotiana tabacum
544482 ALDH6 human
408453 ALDH1 shrew
P27463 ALDH1 chicken
P13601 ALDH1 rat
P15437 ALDH1 horse
P00352 ALDH1 human
P24549 ALDH1 mouse
527682 ALDH1 sheep
537498 ALDH1 bovine
P46329 ALDH (put.) B. subtilis
P12693 ALDH Pseudomonas oleovorance
P30840 ALDH Entomoeba histolitica
P43353 ALDH7 human
ALDH8 human
ALDH3/7/8/10
ALDH3 human
P11883 ALDH3 rat
ALDH10 human
P30839 ALDH10 rat
ALDH9 human
ALDH9
118491 BADH E. coli
145405 BADH E. coli
145404 BADH E. coli
145402 choline ALDH E. coli
114919 choline ALDH E. coli
0.25

FIGURE 6

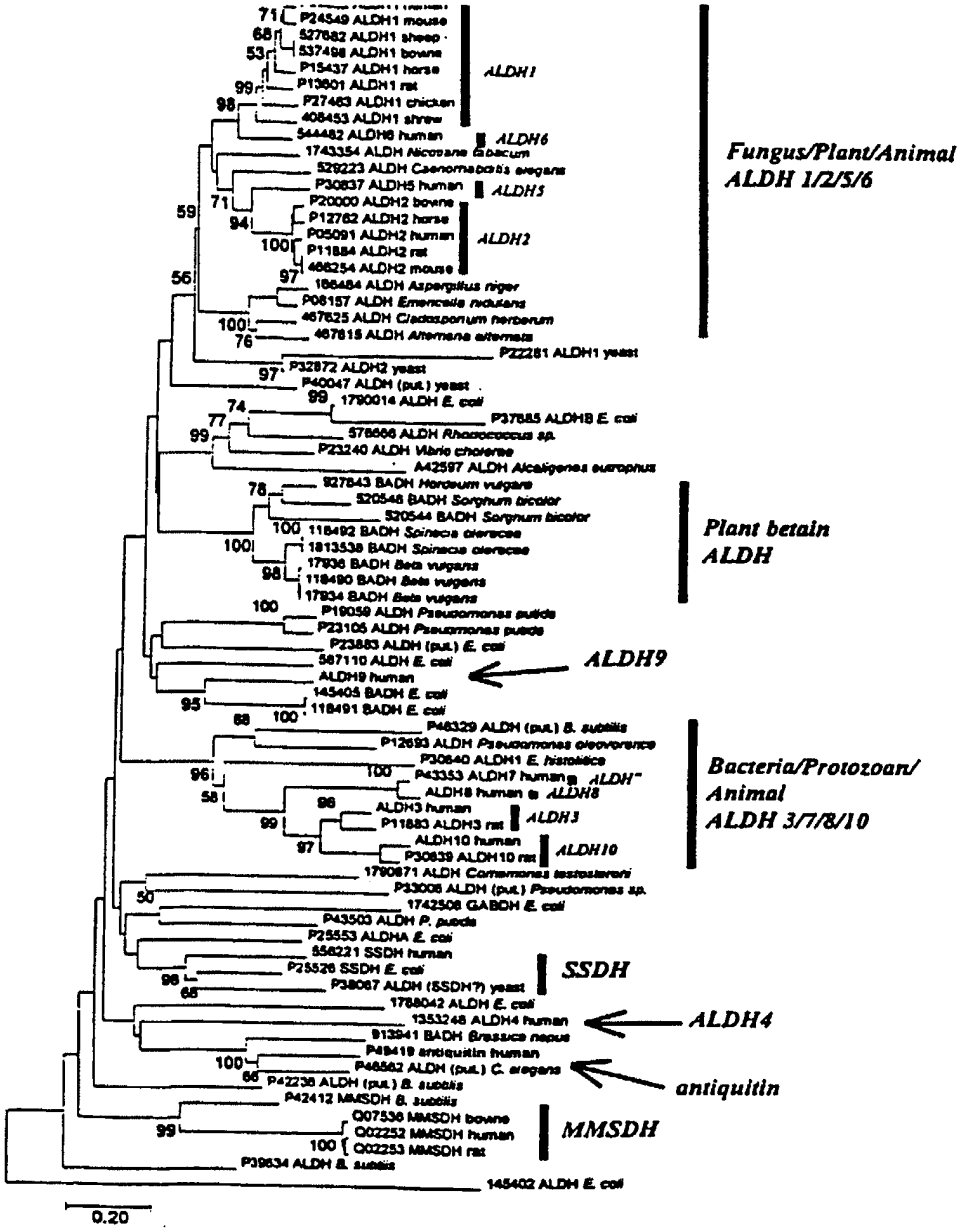
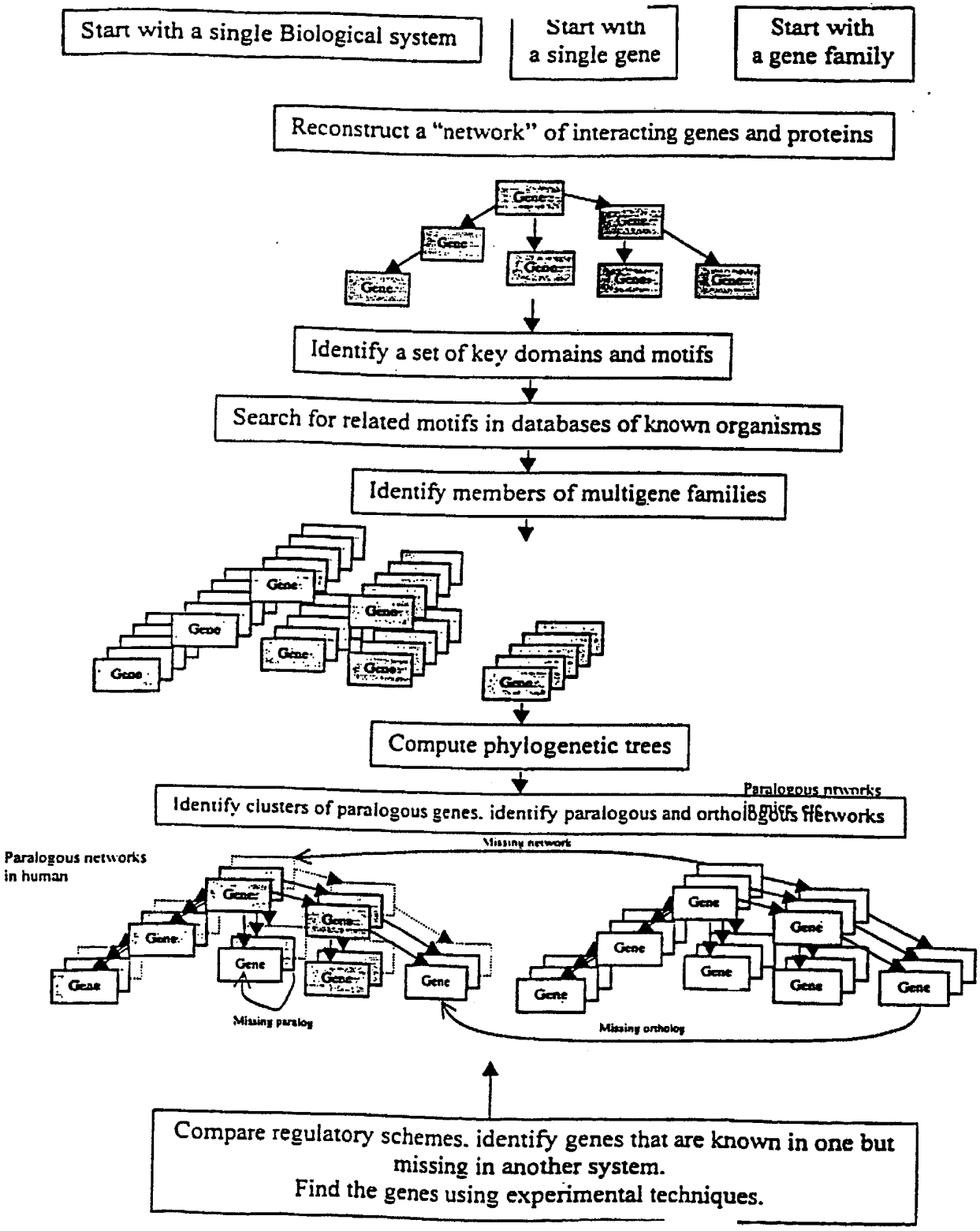

P24549 ALDH1 mouse
527682 ALDH1 sheep
537498 ALDH1 bovine
P15437 ALDH1 horse
P13601 ALDH1 rat
P27463 ALDH1 chicken
408453 ALDH1 shrew
544482 ALDH6 human
1743354 ALDH Nicotiana glauca
529223 ALDH Caenorhabditis elegans
P30837 ALDH5 human
P20000 ALDH2 bovine
P12762 ALDH2 horse
P05091 ALDH2 human
P11884 ALDH2 rat
466254 ALDH2 mouse
166484 ALDH Aspergillus niger
P08157 ALDH Emericella nidulans
467625 ALDH Cladosporium herbarum
467615 ALDH Alternaria alternata
PZ2281 ALDH1 yeast
P32872 ALDH2 yeast
P40047 ALDH (put.) yeast
1790014 ALDH E. coli
P37685 ALDH8 E. coli
578666 ALDH Rhodococcus sp.
P23240 ALDH Vibrio cholerae
A42597 ALDH Alcaligenes eutrophus
927643 BADH Hordeum vulgare
520546 BADH Sorghum bicolor
520544 BADH Sorghum bicolor
118492 BADH Spinacia oleracea
1813538 BADH Spinacia oleracea
17936 BADH Beta vulgaris
118490 BADH Beta vulgaris
17934 BADH Beta vulgaris
P19059 ALDH Pseudomonas putida
P23105 ALDH Pseudomonas putida
P23883 ALDH (put.) E. coli
587110 ALDH E. coli
ALDH9 human
145405 BADH E. coli
118491 BADH E. coli
P46329 ALDH (put.) B. subtilis
P12693 ALDH Pseudomonas oleovorans
P30840 ALDH1 E. histolitica
P43353 ALDH7 human
ALDH8 human
ALDH3 human
P11883 ALDH3 rat
ALDH10 human
P30839 ALDH10 rat
1790871 ALDH Comamonas testosteroni
P33006 ALDH (put.) Pseudomonas sp.
1742508 GABDH E. coli
P43503 ALDH P. putida
P25553 ALDHA E. coli
556221 SSDH human
P25526 SSDH E. coli
P38067 ALDH (SSDH?) yeast
1788042 ALDH E. coli
1353248 ALDH4 human
913941 BADH Brassica napus
P49419 antiquitin human
P46562 ALDH (put.) C. elegans
P42238 ALDH (put.) B. subtilis
P42412 MMSDH B. subtilis
Q07536 MMSDH bovine
Q02252 MMSDH human
Q02253 MMSDH rat
P39834 ALDH B. subtilis
145402 ALDH E. coli
0.20
ALDH1
ALDH6
ALDH5
ALDH2
Fungus/Plant/Animal
ALDH 1/2/5/6
Plant betain
ALDH
ALDH9
Bacteria/Protozoan/
Animal
ALDH 3/7/8/10
ALDH3
ALDH10
SSDH
ALDH4
antiquitin
MMSDH

FIGURE 7

FIGURE 8


Start with a single Biological system
Start with a single gene
Start with a gene family
Reconstruct a "network" of interacting genes and proteins
Identify a set of key domains and motifs
Search for related motifs in databases of known organisms
Identify members of multigene families
Compute phylogenetic trees
Identify clusters of paralogous genes. identify paralogous and orthologous networks
Paralogous networks in human
Missing network
Missing paralog
Missing ortholog
Compare regulatory schemes. identify genes that are known in one but missing in another system.
Find the genes using experimental techniques.

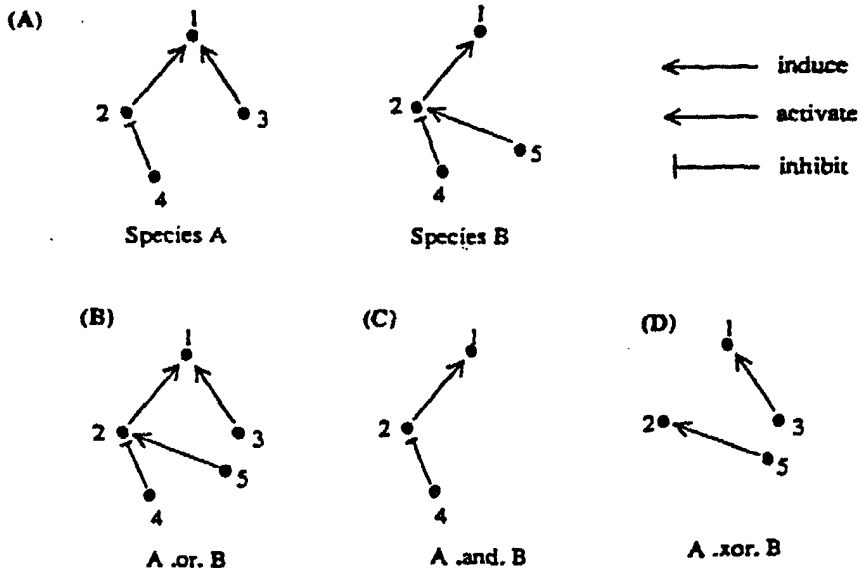

(A)
1
2
3
4
Species A
1
2
5
4
Species B
induce
activate
inhibit
(B)
1
2
3
5
4
A .or. B
(C)
1
2
4
A .and. B
(D)
1
2
3
5
A .xor. B

FIGURE 9

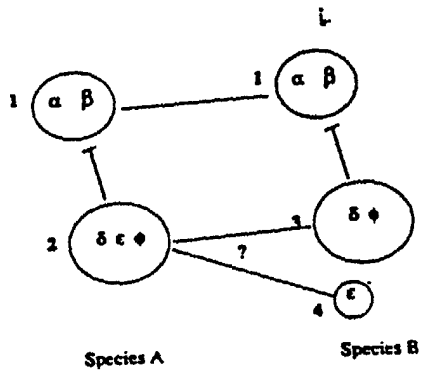


FIGURE 10

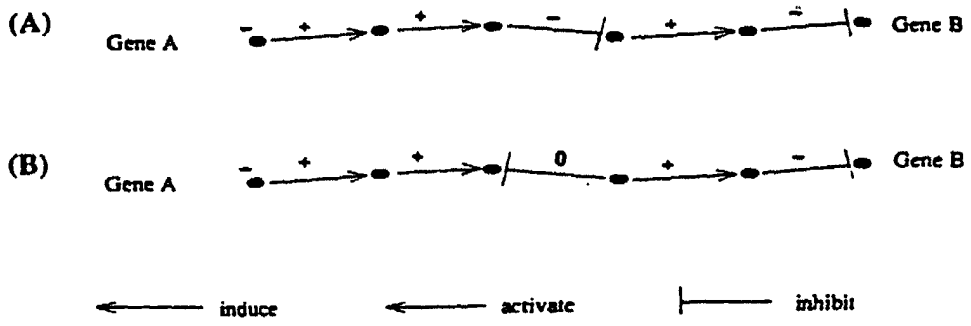


FIGURE 11

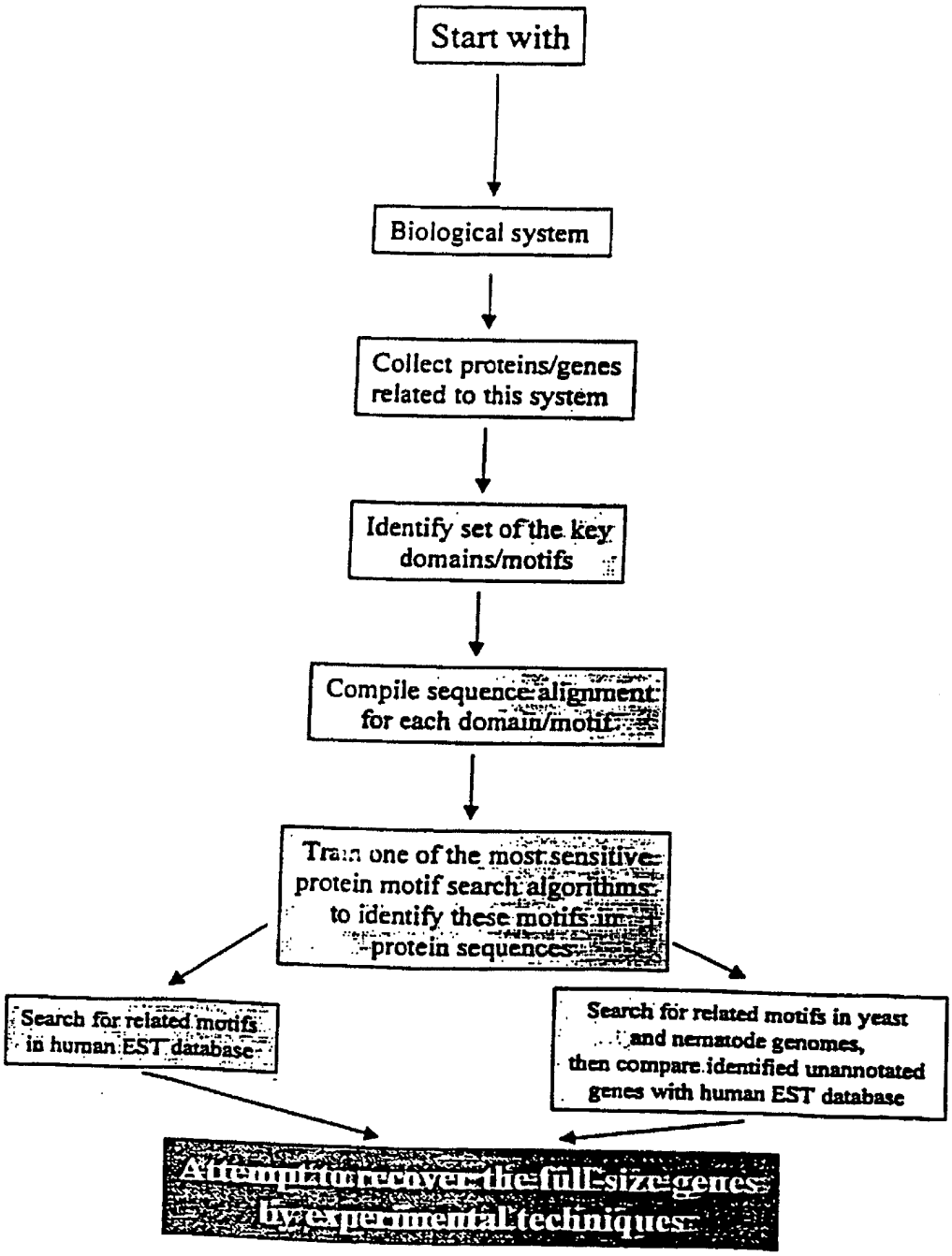

Start with
Biological system
Collect proteins/genes related to this system
Identify set of the key domains/motifs
Compile sequence alignment for each domain/motif
Train one of the most sensitive protein motif search algorithms to identify these motifs in protein sequences
Search for related motifs in human EST database
Search for related motifs in yeast and nematode genomes, then compare identified unannotated genes with human EST database
Attempt to recover the full-size genes by experimental techniques

FIGURE 12

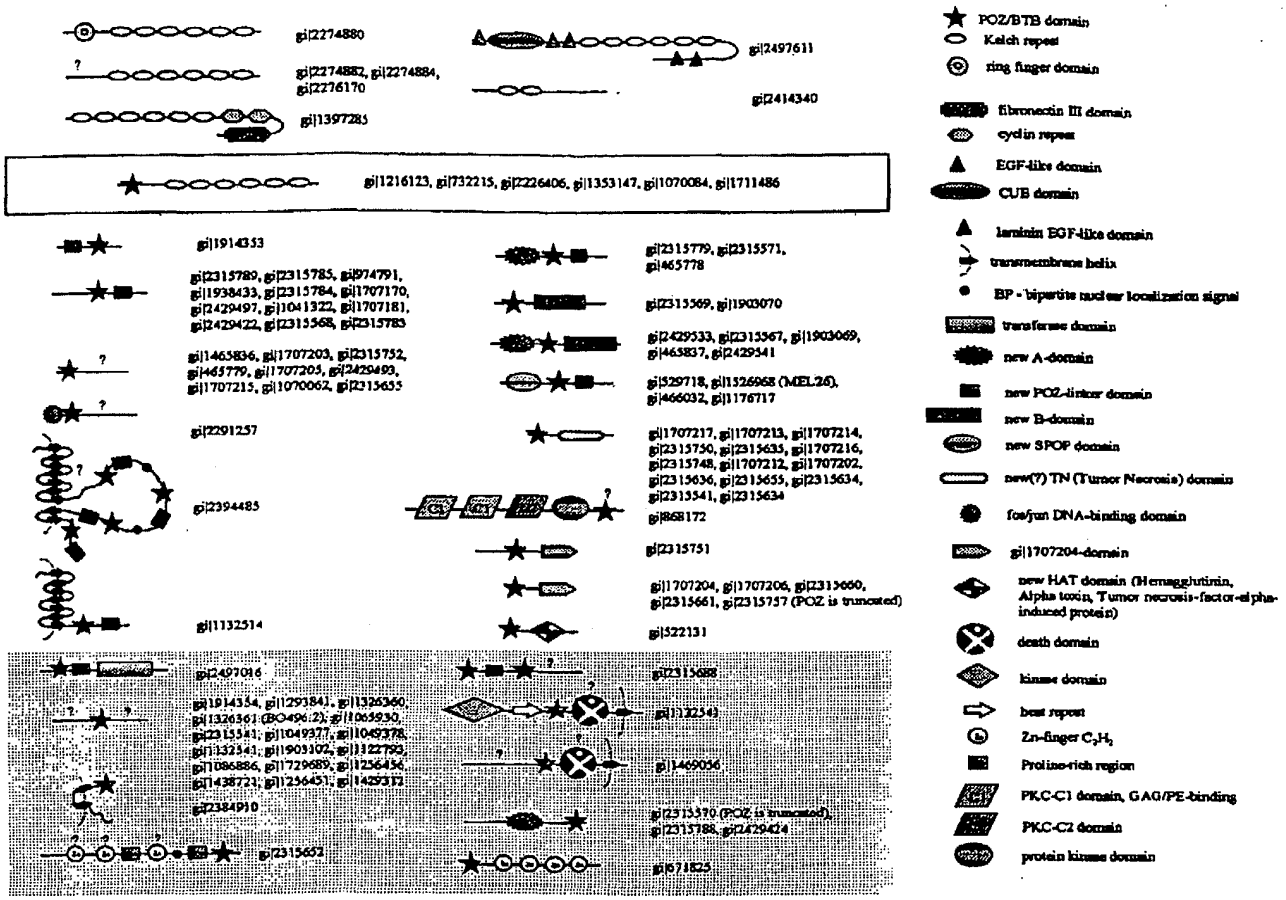

gi|2274880
gi|2274882, gi|2274884, gi|2276170
gi|1397285
gi|2497611
gi|2414340
gi|1216123, gi|732215, gi|2226406, gi|1353147, gi|1070084, gi|1711486
gi|1914353
gi|2315789, gi|2315785, gi|974791, gi|1938433, gi|2315784, gi|1707170, gi|2429497, gi|1041322, gi|1707181, gi|2429422, gi|2315568, gi|2315783
gi|1465836, gi|1707203, gi|2315752, gi|465779, gi|1707205, gi|2429493, gi|1707215, gi|1070062, gi|2315655
gi|2291257
gi|2394485
gi|1132514
gi|2315779, gi|2315571, gi|465778
gi|2315569, gi|1903070
gi|2429533, gi|2315567, gi|1903069, gi|465837, gi|2429541
gi|529718, gi|1326968 (MEL26), gi|466032, gi|1176717
gi|1707217, gi|1707213, gi|1707214, gi|2315750, gi|2315635, gi|1707216, gi|2315748, gi|1707212, gi|1707202, gi|2315636, gi|2315655, gi|2315634, gi|2315541, gi|2315634
gi|868172
gi|2315751
gi|1707204, gi|1707206, gi|2315660, gi|2315661, gi|2315757 (POZ is truncated)
gi|522131
gi|2497016
gi|1914334, gi|1293841, gi|1326360, gi|1326361 (BO496.2), gi|1065930, gi|2315541, gi|1049377, gi|1049378, gi|1132541, gi|1903102, gi|1227593, gi|1086886, gi|1729689, gi|1256456, gi|1438721, gi|1256451, gi|1429312
gi|2384910
gi|2315602
gi|2315688
gi|1322543
gi|1469056
gi|2315370 (POZ is truncated), gi|2315788, gi|2429424
gi|671825
POZ/BTB domain
Kelch repeat
ring finger domain
fibronectin III domain
cyclin repeat
EGF-like domain
CUB domain
laminin EGF-like domain
transmembrane helix
BP - bipartite nuclear localization signal
transferase domain
new A-domain
new POZ-linker domain
new B-domain
new SPOP domain
new(?) TN (Tumor Necrosis) domain
fos/jun DNA-binding domain
gi|1707204-domain
new HAT domain (Hemagglutinin, Alpha toxin, Tumor necrosis-factor-alpha-induced protein)
death domain
kinase domain
beat repeat
Zn-finger C2H2
Proline-rich region
PKC-C1 domain, GAG/PE-binding
PKC-C2 domain
protein kinase domain

Figure 13

>gi|2210766|gb|AA481214|AA481214 aa34e02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815162 5' similar to WP:W07A12.4 CE03795 ;, mRNA sequence [Homo sapiens]
CATGGCTTCCTGGACACCAACCCTGCCATCCGGGAGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAA
AGCTGAACGAGGCCAACCTCAATGTGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACA
GGGCCCCATCCGCTGCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGA
CACAGGGTCCTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGCACCGTCCCGGGTTGCGGGTG
TCCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGAAGATCCTGCCTGTGCT
CTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGGCCTTCAAGGCA

>gi|1349211|gb|W51957|W51957 zc45f01.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325273 5', mRNA sequence [Homo sapiens]
CCTTCGAGTTCGGCAATGCTGGGGCCGTTGTCCTCACGCCCCTCTTCAAGGTGGGCAAGTTCCTGAGCGC
TGAGGAGTATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGCGC
ATCCGNCTCCTGCAGCAGATGGAGCAGTTCATCCAGTACCTTGACGAGCCAACAGTCAACACCCAGATCT
TCCCCCACGTCGTACATGGCTTCCTGGACACCAACCCTGCCATCCGGGAGCAGACGGTCAAGTCCATGCT
GCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATGTGGAGCTGATGAAGCACTTTGCACGGCTACAG
GCCAAGGATGAACAGGGCCCCATCCGCTGCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCA
GTGCTAGCACCAGACACAGGGTCCTTACCTCTG

Figure 14A

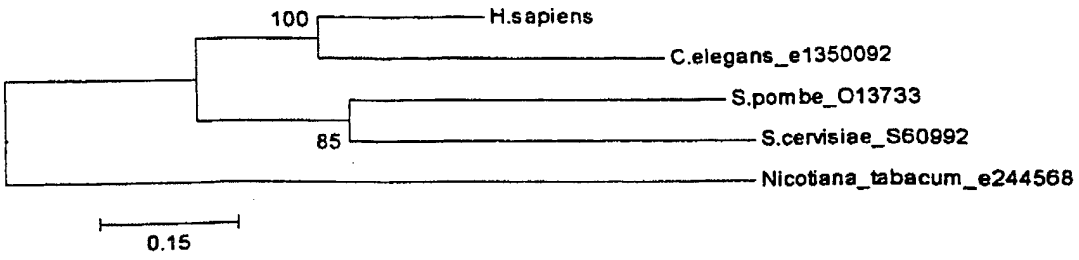

100
H.sapiens
C.elegans_e1350092
S.pombe_O13733
85
S.cervisiae_S60992
Nicotiana_tabacum_e244568
0.15

Figure 14B

```
BASE COUNT      405 a    545 c    493 g    278 t      6 others
ORIGIN
        1 cagccgaagc amgcaaaaat tcttccagga gctgagcaag agcctggacg cattccctga
       61 ggayttctgt cggcacaagg tgctgcccca gctgctgacc gccttcgagt tcggcaatgc
      121 tggggccgtt gtcctcacgc ccctcttcaa ggtgggcaag ttcctgagcg ctgaggagta
      181 tcagcagaag atcatccctg tggtggtcaa gatgttctca tccactgacc gggccatgcg
      241 catccgcctc ctgcagcaga tggagcagtt catccagtac cttgacgagc caacagtcaa
      301 cacccagatc ttcccccacg tcgtacatgg cttcctggac accaaccctg ccatccggga
      361 gcagacggtc aagtccatgc tgctcctggc cccaaagctg aacgaggcca acctcaatgt
      421 ggagctgatg aagcactttg cacggctaca ggccaaggat gaacagggcc ccatccgctg
      481 caacaccaca gtctgcctgg gcaaaatcgg ctcctacctc agtgctagca ccagacacag
      541 ggtccttacc tctgccttca gccgagccac tagggacccg tttgcaccgt cccgggttgc
      601 gggtgtcctg ggctttgctg ccacccacaa cctctactca atgaacgact gtgcccagaa
      661 gatcctgcct gtgctctgcg gtctcactgt agatcctgag aaatccgtgc gagaccaggc
      721 cttcaaggcm wttcggagct tcctgtccaa attggagtct gtgtcggagg acccgaccca
      781 gctggaggaa gtggagaagg atgtccatgc agcctccagc cctggcatgg gaggagccgc
      841 agctagctgg gcaggctggg cgtgaccggg gtctcctcac tcacctccaa gctgatccgt
      901 tcgcacccaa ccactgcccc aacagaaacc aacattcccc aaagacccac gcctgaagga
      961 gttcctgccc cagcccccac ccctgttcct gccaccccta caacctcagg ccactgggag
     1021 acgcaggagg aggacaagga cacagcagag gacagcagca ctgctgacag atgggacgac
     1081 gaagactggg gcagcctgga gcaggaggcc gagtctgtgc tggcccagca ggacgactgg
     1141 agcaccgggg gccaagtgag ccgtgctagt caggtcagca actccgacca caaatcctcc
     1201 aaatccccag agtccgactg gagcagctgg gaarctgagg gctcctggga acagggctgg
     1261 caggagccaa gctcccagga gccacctyct gacggtacac ggctggccag cgagtataac
     1321 tggggtggcc cagagtccag cgacaagggc gacccttcg ctaccctgtc tgcacgtccc
     1381 agcacccagc cgaggccaga ctcttggggt gaggacaact gggagggcct cgagactgac
     1441 agtcgacagg tcaaggctga gctggcccgg aagaagcgcg aggagcggcg gcgggagatg
     1501 gaggccaaac gcgccgagag gaaggtgcca agggccccat gaagctggga gcccggaagc
     1561 tggactgaac cgtggcggtg gcccttcccg gctgcggaga gcccgcccca cagatgtatt
     1621 tattgtacaa accatgtgag cccggccgcc cagccaggcc atctcacgtg tacataatca
     1681 gagccacaat aaattctatt tcacaaaaaa aaaaaaaaaa aaaaaaa
//
```

Figure 14C

```
                  5        10        15        20        25        30
  1  S R S X Q K F F Q E L S K S L D A F P E D F C R H K V L P Q
 31  L L T A F E F G N A G A V V L T P L F K V G K F L S A E E Y
 61  Q Q K I I P V V V K M F S S T D R A M R I R L L Q Q M E Q F
 91  I Q Y L D E P T V N T Q I F P H V V H G F L D T N P A I R E
121  Q T V K S M L L L A P K L N E A N L N V E L M K H F A R L Q
151  A K D E Q G P I R C N T T V C L G K I G S Y L S A S T R H R
181  V L T S A F S R A T R D P F A P S R V A G V L G F A A T H N
211  L Y S M N D C A Q K I L P V L C G L T V D P E K S V R D Q A
241  F K A X R S F L S K L E S V S E D P T Q L E E V E K D V H A
271  A S S P G M G G A A A S W A G W A
```

Figure 14D

>sp|P15533|RPT1_MOUSE DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR (J03776) rpt-1r [Mus musculus] Length = 353

Score = 92.0 bits (237), Expect = 6e-20

```
Query 194 VMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILEGSVRNSMWRPAPFKCPTCRK 373
          V+E+++E++TCPIC  L  +P    C+H+FC+ C+    E S RN+        CP CR
Sbjct 5   VLEMIKEEVTCPICLELLKEPVSADCNHSFCRACITLNYE-SNRNT---DGKGNCPVCRV 60

Query 374 ETSATGINSLQVNYSLKGIVEKYNKIKISP----KMPVCKGHMGQPLNIFCLTDMQLICG 541
            +L+ N  +  IVE+    K  P    K+ +C  H G+ L +FC  DM +IC
Sbjct 61  PYP---FGNLRPNLHVANIVERLKGFKSIPEEEQKVNICAQH-GEKLRLFCRKDMMVICW 116

Query 542 ICATRGEHTKHVFCSIEDAYAQERDAFESLFQSF-------ETWRRGDALSRLDTMETSK 700
          +C    EH  H    IE+   + ++  +              + W+    L R+D
Sbjct 117 LCERSQEHRGHQTALIEEVDQEYKEKLQGALWKLMKKAKICDEWQDDLQLQRVDW----- 171

Query 701 RKSLQLMTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMKLAVMQAYDPEINKL 862
             +Q+   + + V+  F+ L+  LD K+NE L   +  K  VM+  +   N+L
Sbjct 172 ENQIQI---NVENVQRQFKGLRDLLDSKENEELQKLKKEKKEVMEKLEESENEL 222
```

Homology covers ring finger, B-box and the beginning of coiled coil domain in the CLL ring finger protein

Figure 15

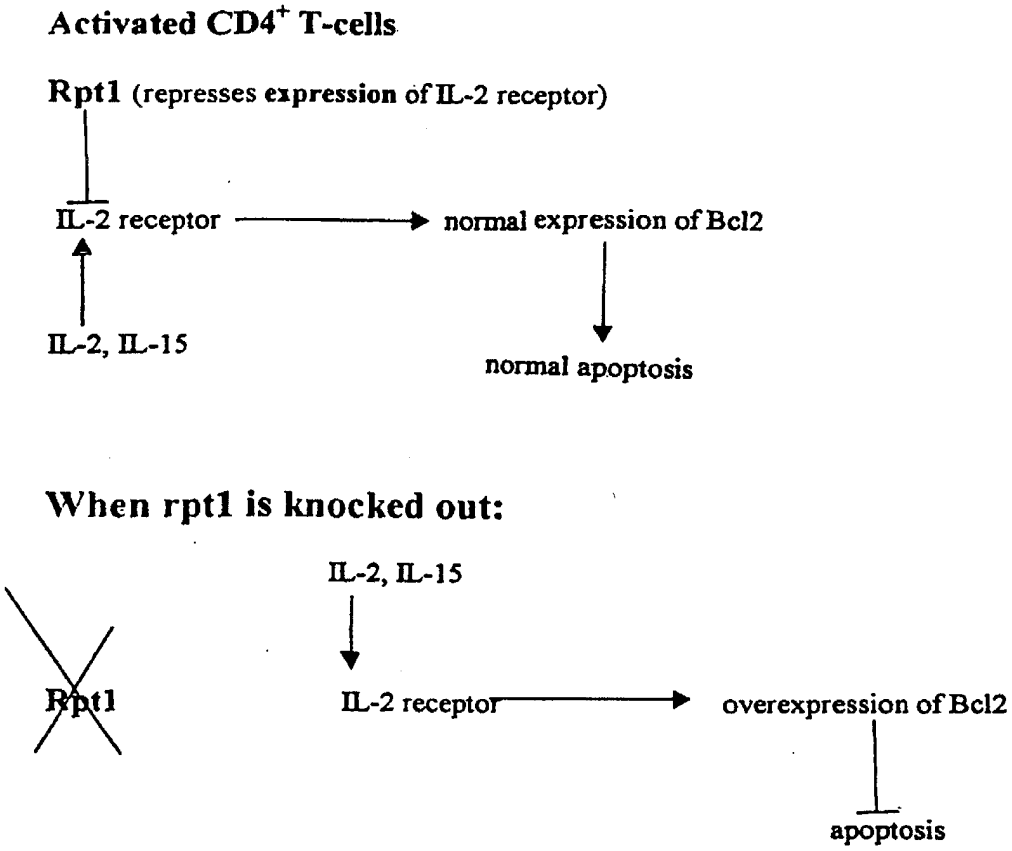

Activated CD4+ T-cells
Rpt1 (represses expression of IL-2 receptor)
IL-2 receptor
normal expression of Bcl2
IL-2, IL-15
normal apoptosis
When rpt1 is knocked out:
IL-2, IL-15
Rpt1
IL-2 receptor
overexpression of Bcl2
apoptosis

Figure 16

```
TBLASTN 2.0.8 [Jan-05-1999]


Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2137498|Mad3m
         (205 letters)


gb|AA278224|AA278224 zs77e05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703520 5'
           similar to TR:G1184157 G1184157 MAX-INTERACTING
           TRANSCRIPTIONAL REPRESSOR. ;
           Length = 430

 Score =  209 bits (526), Expect = 1e-53
 Identities = 104/124 (83%), Positives = 116/124 (92%), Gaps = 1/124 (0%)
 Frame = +2

Query: 1   MEPVASNIQVLLQAAEFLERREREAEHGYASLCPHHSPGTVCRRRKPPLQAPGALNSGRS 60
           MEP+ASNIQVLLQAAEFLERREREAEHGYASLCPH SPG + RR+K P QAPGA +SGRS
Sbjct: 56  MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRS 235

Query: 61  VHNELEKRRRAQLKRCLEQLRQQMPLGVDCTRYTTLSLL-RARVHIQKLEEQEQQARRLK 119
           VHNELEKRRRAQLKRCLE+L+QQMPLG DC RYTTLSLL RAR+HIQKLE+QEQ+AR+LK
Sbjct: 236 VHNELEKRRRAQLKRCLERLKQQMPLGGDCARYTTLSLLRRARMHIQKLEDQEQRARQLK 415

Query: 120 EKLRS 124
           E+LR+
Sbjct: 416 ERLRT 430


dbj|C02407|C02407 HUMGS0012279, Human Gene Signature, 3'-directed cDNA sequence.
           Length = 348

 Score = 97.5 bits (239), Expect = 6e-20
 Identities = 51/63 (80%), Positives = 56/63 (87%)
 Frame = +3

Query: 125 KQQSLQQQLEQLQGLPGARERERLRADSLDSSGLSSERSDSDQEDLEVDVENLVFGTETE 184
           KQQSLQ+   QL+GL GA ERERLRADSLDSSGLSSERSDSDQE+LEVDVE+LVFG E E
Sbjct: 45  KQQSLQRXWMQLRGLAGAAERERLRADSLDSSGLSSERSDSDQEELEVDVESLVFGGEAE 224

Query: 185 LLQ 187
           LL+
Sbjct: 225 LLR 233
```

Figure 17A

```
BASE COUNT      130 a    234 c    258 g    106 t      5 others
ORIGIN
        1 cagccgcttg ctccggccgg caccctaggc cgcagtccgc caggctgtcg ccgacatgga
       61 acccttggcc agcaacatcc aggtcctgct gcaggcggcc gagttcctgg agcgccgtga
      121 gagagaggcc gagcatggtt atgcgtccct gtgcccgcat cgcagtccag gccccatcca
      181 caggaggaag aagcgacccc cccaggctcc tggcgcgcag gacagcgggc ggtcagtgca
      241 caatgaactg gagaagcgca ggagggccca gttgaagcgg tgcctggagc ggctgaagca
      301 gcagatgccc ctgggcggcg actgtgcccg gtacaccacg ctgagcctgc tgcgccgtgc
      361 caggatgcac atccagaagc tggaggatca ggagcagcgg gcccgacagc tcaaggagag
      421 gctgcgcaca aagcagcaga gcctgcagcg gcantggatg cagctccggg ggctggcagg
      481 ngcggccgag cgggagcgnc tgcgggcgga cagtctggac tcctcaggcc tctcctctga
      541 gcgctcagac tcagaccaag aggagctgga ggtggatgtg gagagcctgg tgtttggggg
      601 tgaggccgag ctgctgcggg gcttcgtcgc cggccaggag cacagctact cgcacgtcgg
      661 cggcgcctgg ctatgatgtt cctcacccan ggcgggcctc tgccctctta ctcgttgccc
      721 aagcccactt tnc
```

Figure 17B

C

>*Mad*3h(Putative)
MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRSVHNELEKRRRAQLK
RCLERLKQQMPLGGDCARYTTLSLLRRARMHIQKLEDQEQRARQLKERLRTKQQSLQRXWMQLRGLAGAAERER
LRADSLDSSGLSSERSDSDQEELEVDVESLVFGGEAELLRGFVAGQEHSYSHVGGAWL

D

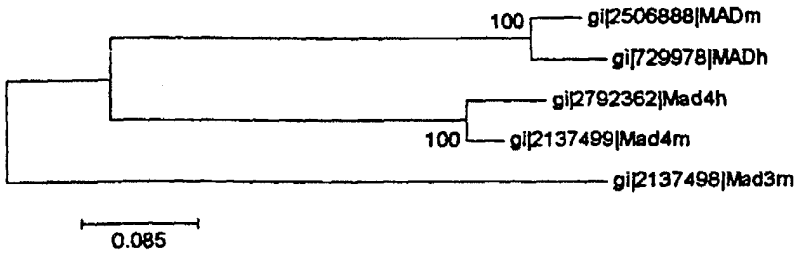
```
gi|2506888|MADm     MATAVGMNIQLLLEAADYLERREREAEHGYASMLPYS-KDRDAFKRRNKPKKNST--SSRSTHNEMEKNRRAHLRLCLEKLKGLVPLGPESSRHTTLSLL
gi|729978|MADh      MAAAVRMNIQMLLEAADYLERREREAEHGYASMLPYNNKDRDALKRRNKSKKNNS--SSRSTHNEMEKNRRAHLRLCLEKLKGLVPLGPESSRHTTLSLL
gi|2792362|Mad4h    ---MELNSLLILLEAAEYLERRDREAEHGYASVLPFDGDFAREKTKAAGLVRKAP--NNRSSHNELEKHRRAKLRLYLEQLKQLVPLGPDSTRHTTLSLL
gi|2137499|Mad4m    ---MELNSLLLLLEAAEYLERRDREAEHGYASHLPFDGDFARKKTKTAGLVRKGP--NNRSSHNELEKHRRAKLRLYLEQLKQLGPLGPDSTRHTTLSLL
gi|2137498|Mad3m    -MEPVASNIQVLLQAAEFLERREREAEHGYASLCPHHSPGTVCRRRKPPLQAPGALNSGRSVHNELEKRRRAQLKRCLEQLRQQMPLGVDCTRYTTLSLL
Mad3h Putative      -MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRSVHNELEKRRRAQLKRCLERLKQQMPLGGDCARYTTLSLL

gi|2506888|MADm     TKAKLHIKKLEDCDRKAVHQIDQLQREQRHLKRRLEKLGAERTR--------MDSVG-SVVSSERSDSDREELDVDVDVDVDVDVEGTDYLNGDLGWSSS-
gi|729978|MADh      TKAKLHIKKLEDCDRKAVHQIDQLQREQRHLKRQLEKLGIERIR--------MDSIG-STVSSERSDSDRE--------EIDVDVESTDYLTGDLDWSSSS
gi|2792362|Mad4h    KRAKVHIKKLEEQDRRALSIKEQLQQEHRFLKRRLEQLSVQSVER-----VRTDSTG-SAVSTD--DSEQE-----------VDIEGMEFGPGELDSVGS-
gi|2137499|Mad4m    K-AKMHIKKLEEQDRRALSIKEQLQREHRFLKRRLEQLSVQSVR------VRTDSTG-SAVSTD--DSEQE-----------VDIEGMEFGPGELDSAGS-
gi|2137498|Mad3m    R-ARVHIQKLEEQEQQARRLKEKLRSKQQSLQQQLEQLQGLPGARERERLRADSLDSSGLSSERSDSDQE--------DLEVDVENLVFG-TETELLQSF
Mad3h Putative      RRARMHIQKLEDQEQRARQLKERLRTKQQSLQRXWMQLRGLAGAAERERLRADSLDSSGLSSERSDSDQE--------ELEVDVESLVFG-GEAELLRGF

gi|2506888|MADm     VSDSDERGSMQSLG-SDEGYSSATVKRAKLQQGHKAGLGL
gi|729978|MADh      VSDSDERGSMQSLG-SDEGYSSTSHKRIKLQQSHKACLGL
gi|2792362|Mad4h    SSDADDHYSLQSGTGGDSGFGPHCRRLGRPALS-------
gi|2137499|Mad4m    SSDADDHYSLQSSGCSDSSYGHPCRRPGCPGLS-------
gi|2137498|Mad3m    SAGRERSYSRSTCAWL-------------------------
Mad3h Putative      VAGQERSYSHVGGAWL-------------------------
```

Figure 17 C-D

A.



B.

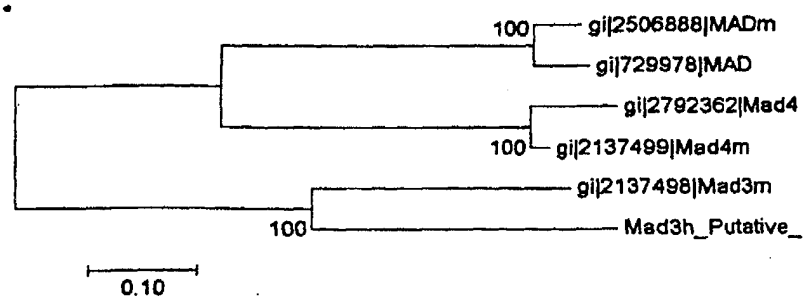


Figure 18. A-B

```
% lexsemsub.pl
% lexsemsub.pat
% revised  March 17, 2000
%           LEXICON OF SUBSTANCES AND STRUCTURES
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
:-multifile(phrase/5).
:-multifile(wdef/3).
:-unknown(_,fail).
phrase('[',protein, ['[',gamma,']','-',aminobutyric, acid, a], 'GA
BAA', r).  % ?
phrase('[',smallmolecule, ['[',zeta,']',1, subunit], '[zeta]1 subu
nit', r).  % ?
phrase(116, protein,[116,'-',kd,fyn,'-',associated,protein],'116-k
D Fyn-associated protein',r).
phrase(116, protein,[116,'-',kd,protein], '116-kd protein',r).
phrase(3,protein, [3,'-',kinase,'-',akt],  '3-kinase-Akt',r).
phrase(ability, affirmation, [ability, to], [], r).
phrase(agc,protein, [agc, protein, kinases], 'AGC', r).
phrase(akt,protein, [akt, mutant], 'Akt mutant', r).
phrase(alternative,substance,[alternative,ntf],'alternative NTF',r
).
phrase(antibody, protein,[antibody,to,phosphotyrosine],'anti-phosp
hotyrosine',r).
phrase(antigen, complex,[antigen,receptor], 'antigen receptor',r).
phrase(ap, protein, [ap,'-',1],'AP-1',r).
phrase(aspargine,site,[aspargine,'-',141],'aspargine-141',r).
phrase(b, cell, [b,cell], 'B cell', r).
phrase(b, cell, [b,cells], 'B cell', r).
phrase(b, species,[b,lymphoblastoid,cells], 'B lymphoblastoid cell
s',r).
phrase(b,cell,[b,lymphoblastoid,cells], 'B lymphoblastoid cells',r
).
phrase(b7, protein, [b7,'-','1'], 'B7-1',r).
phrase(bcl,protein,[bcl,'-',2],'Bcl-2',r).
phrase(c, protein, [c,'-',jun] , 'c-Jun',r).
phrase(camk, protein, [camk, iv], 'CaMK IV',r).
phrase(casp, protein,[casp,'-',3], 'caspase-3',r).
phrase(caspase,protein,[caspase,'-',3,family,protease], 'caspase-3
 family protease',r).
phrase(caspase,protein,[caspase,'-',3,precursor],'caspase-3 precur
sor',r).
phrase(caspase,protein,[caspase,'-',3],'caspase-3',r).
phrase(caspase,protein,[caspase,-,3],'caspase-3',r).
```

Appendix A

```
phrase(caspase,protein,[caspase,'-',6],'caspase-6',r).
phrase(caspase,protein,[caspase,'-',7],'caspase-7',r).
phrase(catalytic, domain, [catalytic, domain], 'catalytic domain',
r).
phrase(cleavage,site,[cleavage,site],'cleavage site',r).
phrase(cleavage,substance,[cleavage,products],'cleavage products',
r).
phrase(cooh,substance, [cooh,'-',terminal,fragment], 'COOH-termina
l fragment',r).
phrase(crk,protein,[crk,proteins], 'crk proteins',r0.
phrase(crkl, complex,[crkl,'-',c3g,complex],'crkl-c3g complex',r).
phrase(dcp,protein,[dcp,-,1],'DCP-1',r).
phrase(did, negation, [did, not], not, r).
phrase(ebv,species, 'Epstein-Barr virus',r).
phrase(epstein, species, [epstein,'-',barr,virus],'Epstein-Barr vi
rus',r).
phrase(familial,disease,[familial,alzheimer,'''',s,disease],'famil
ial Alzheimer''''s disease',r).
phrase(gene, gene, [gene,encoding,interleukin,'-',2],'gene encodin
g interleukin-2', r).
phrase(gst, protein, [gst,'-','fyn','-',sh2], 'GST-Fyn-SH2',r).
phrase(gst, protein, [gst,'-','fyn','-',sh3], 'GST-Fyn-SH3',r).
phrase(gtp, complex,[gtp,exchange,of,rap1],'GTP exchange of Rap1',
r).
phrase(guanidine, protein, [guanidine,nucleotide,'-',releasing,fac
tor,c3g],'guanidine nucleotide-releasing factor C3G',r).
phrase(guanidine, smallmolecule, [guanidine,nucleotide],'guanidine
 nucleotide',r).
phrase(guanosine, smallmolecule,[guanosine,triphosphate],'guanosin
e triphosphate',r).
phrase(guanosine,smallmolecule,[guanosine,diphosphate],'guanosine
diphosphate',r).
phrase(h4,cell,[h4,cell,line], 'H4 cell line',r).
phrase(h4,cell,[h4,human,neuroglioma,cells], 'H4,human,neuroglioma
,cells',r).
phrase(ha, protein, [ha, '-', '[',delta,']',phpkb],'HA-[Delta]PHPK
B',r).
phrase(hla, protein, [hla,'-',dr7], 'HLA-DR7',r).
phrase(i, protein, [i, '[',kappa, ']',b,'-','[',beta,']'],   'I[ka
ppa]B-[beta]',r).
phrase(i,protein, [i, '[',kappa, ']',b,'-','[',alpha,']'],  'I[kap
pa]B-[alpha]',r).
phrase(i,protein, [i, '[',kappa, ']',b], 'I[kappa]B',r).
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phrase(ice,protein,[ice,'/',ced,'-',3],'ICE/Ced-3',r).
phrase(il, gene, [il,'-',2,gene], 'gene encoding interleukin-2', r
).
phrase(il, protein, [il,'-',2], 'interleukin-2',r).
phrase(in, interm, [in, the, case, of],[], r).
phrase(in,state,[in,the,anergic,state], inactive,r).
phrase(inducible, cell, [inducible,h4,cell], 'inducible H4 cell',r
).
phrase(interleukin, protein, [interleukin,'-',2],r).
phrase(interleukin, protein,[interleukin, '-', 3], 'interleukin-3
',r).
phrase(interleukin,protein,[interleukin,'-',1,beta,converting,enzy
me], 'interleukin-1 beta converting enzyme',r).
phrase(jurkat, cell, [jurkat, cell], 'Jurkat cell', r).
phrase(jurkat, cell, [jurkat, cells], 'Jurkat cell', r).
phrase(kif3a,protein,[kif3a,'/',3,b],'KIF3A/3B',r).
phrase(lbl, cell, [lbl,'-',drf, cells], 'LBL-DR7 cells',r).
phrase(lbl,cell,[lbl,'-',dr7,cells],'LBL-DR7 cells',r).
phrase(let, protein, [let,'-',23], 'Let-23', r).
phrase(may, probability,[may, be], possible, r).
phrase(myc, protein, [myc, '-', p70s6kd3e], 'Myc-p70s6kD3E',r).
phrase(myc, protein, [myc, '-', pdk1], 'Myc-PDK1',r).
phrase(myc,protein,[myc,'-',p70s6k],'Myc-p70s6k',r).
phrase(myc,protein,[myc,'-',p70s6ke389d3e], 'Myc-p70s6kE389D3E',r)
.
phrase(myr, protein,[myr,'-',akt], 'Myr-Akt',r).
phrase(n,protein, [n,'-',methyl,'-',d,'-',aspartate, receptor], 'N
MDAR', r).
phrase(n,protein, [n,'-',methyl,'-',d,'-',aspartate], 'NMDA').
phrase(native, cell, [native,h4,cell],'native H4 cell',r).
phrase(nf, protein, [nf,'-','[',kappa,']',b], 'NF-[kappa]B',r).
phrase(nh2, site, [nh2,'-',terminal], 'NH2-terminal',r).
phrase(nh2,substance,[nh2,'-',terminal,fragment], 'NH2-terminal fr
agment',r).
phrase(nih, cell,[nih,'-',3,t3,fibroblasts], 'NIH-3T3 fibroblasts'
, r).
phrase(nih,cell,[nih,'-','3t3', fibroblasts],'NIH-3T3 fibroblasts'
,r).
phrase(normal,substance,[normal,ntf],'normal NTF',r).
phrase(nuclear, protein, [nuclear, factor, kappa, b],'NF-[kappa]B'
, r).
phrase(p150Glued,protein,[p150Glued,-,arp1],'p150Glued-Arp1',r).
phrase(phosphate,phosphorylate2, [phosphate, incorporated, into],
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phosphorylate,r).

phrase(phosphatidylinositol, smallmolecule,[phosphatidylinositol,1
,',',4,',',5,'-',triphosphate], 'phosphatidylinositol 1,4,5-tripho
sphate',r).
phrase(phosphoinositide, protein, [phosphoinositide,'-',dependent,
 protein, kinase], 'PDK1',r).
phrase(phospholipase, protein, [phospholipase,c,'-',1],'phospholip
ase C-1', r).
phrase(poly,protein,[poly,'(',adp,'-',ribose,')',polymerase],'poly
(ADP-ribose) polymerase',r).
phrase(polyvinylidene, structure,[polyvinylidene, difluoride, memb
ranes],'polyvinylidene difluoride membranes',r).
phrase(presenilin, protein,[presenilin,1],'presenilin 1',r).
phrase(presenilin,protein,[presenilin,2],'presenilin,2',r).
phrase(productively, state,[productively,stimulated],active,r).
phrase(protein, protein, [protein,tyrosine,kinase],'protein tyrosi
ne kinase', r).
phrase(protein,protein,[protein,kinase,c],'protein kinase C',r).
phrase(ps2,substance,[ps2,'-',ctf],'presenilin 2 COOH-terminal fra
gment',r).
phrase(ps2,substance,[ps2,cleavage,fragment], 'presenilin 2 cleava
ge fragment', r).
phrase(pvdf, structure, [pvdf, membranes],'polyvinylidene difluori
de membranes',r).
phrase(raf, protein, [raf,'-',1], 'Raf-1', r).
phrase(raf,protein,[raf,'-',1], 'Raf-1',r).
phrase(rap1,complex,[rap1,'-',gtp], 'Rap1-GTP',r).
phrase(requirement, need2, [requirement, for], need,r).
phrase(ser, smallmolecule, [ser, 19], 'Ser 19',r).
phrase(ser, smallmolecule, [ser, 23], 'Ser 23',r).
phrase(serine, substance, [serine, residues], 'serine residues', r
).
phrase(src, domain, [src, homology, 2], 'Src homology 2',r).
phrase(src, domain, [src, homology, 3], 'Src homology 3',r).
phrase(srebp,protein,[srebp,'-',1], 'sterol-regulatory element bin
ding protein 1',r).
phrase(srebp,protein,[srebp,'-',2], 'sterol-regulatory element bin
ding protein 2',r).
phrase(sterol,protein,[sterol,'-',regulatory,element,binding,prote
in,1],'sterol-regulatory element binding protein 1',r).
phrase(sterol,protein,[sterol,'-',regulatory,element,binding,prote
in,2],'sterol-regulatory element binding protein 2',r).
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phrase(t, cell, [t,'-',dr7], 't-DR7',r).
phrase(t, cell, [t,'-',drt,'/',b7,'-',1],'t-DR7/B7-1',r).
phrase(t, cell, [t,cell], 'T cell',r).
phrase(t, cell, [t,cells], 'T cell',r).
phrase(t, complex,[t,'-',cell,receptor],'T-cell receptor',r).
phrase(t,cell,[t,'-',dr7, cells],'t-DR7 cells',r).
phrase(t,cell,[t,'-',dr7,'/',b7,'-',1], 't-DR7/B7-1',r).
phrase(t,complex,[t,'-',cell,antigen,receptor],'T-cell antigen rec
eptor',r).
phrase(threonine, aminoacid, [threonine, 229], 'threonine 229', r)

phrase(transcription, protein,[transcription, factor], 'transcript
ion factor',r).
phrase(trypan,smallmolecule,'trypan blue',r).
phrase(wt,protein, [wt, akt], 'WT Akt',r).
phrase(zap, protein, [zap,'-',70],'ZAP-70',r).
phrase(zdevd,smallmolecule,[zdevd,'-',fmk],'zDEVD-fmk',r).
phrase(il, protein,[il,'-',3],' interleukin-3',r).
wdef(ab, complex, antibody).
wdef(actin,protein,actin).
wdef(activated, state, active).
wdef(active, state, active).
wdef(ad,disease,'Alzheimer''''s disease').
wdef(agc,protein, 'AGC').
wdef(akt, protein, 'AKT').
wdef(anergic,state,inactive).
wdef(anergic,state,inactive).
wdef(anergy,state,inactive).
wdef(antibody,complex,antibody).
wdef(antigen, substance, antigen).
wdef(aop, protein, 'Aop').
wdef(apoptosis,process,apoptosis).
wdef(bad, protein, 'BAD').
wdef(c3g, protein, 'C3G').
wdef('ca2+', smallmolecule,'Ca2+').
wdef(cas, protein, 'Cas').
wdef(caspase,protein,caspase).
wdef(caspase,protein,caspase).
wdef(cbl, protein, 'Cb1').
wdef(ccrsrh,protein,'CCRSrh').
wdef(cd28, protein, 'CD28').
wdef(cells, structure, cell).
wdef(cholesterol,smallmolecule,cholesterol).
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wdef(cpp32,protein,'CPP32').
wdef(crkl, protein, 'CrkL').
wdef(ctf,substance,'COOH-terminal fragment').
wdef(cytokine, smallmolecule, cytokine).
wdef(cytosol, structure, cytosol).
wdef(djnk,protein, 'DJNK').
wdef(djun, protein, 'DJun').
wdef(dynamitin,protein,dynamitin).
wdef(erk, protein, 'ERK').
wdef(eto,smallmolecule,'ETO').
wdef(etoposide,smallmolecule,etoposide).
wdef(fad,disease,'familial Alzheimer''''s disease').
wdef(fyn, protein, 'Fyn').
wdef(gdp, smallmolecule,'GDP').
wdef(gelsolin,protein,gelsolin).
wdef(gp120,protein,'gp120').
wdef(grb2, protein, 'Grb2').
wdef(gst, protein, 'glutathione S-transferase').
wdef(gtp, smallmolecule,'GTP').
wdef(hsp70,protein,'HSP70').
wdef(human, species, human).
wdef(ikk, protein, 'IKK').
wdef(inactivated, state, inactive).
wdef(inactive,state, inactive).
wdef(jnk, protein, 'JNK').
wdef(jnk, protein, 'JNK').
wdef(jnk2, protein,' JNK2').
wdef(kap3,protein,kap3).
wdef(kdakt, protein, 'KDAkt').
wdef(kinase,protein, kinase).
wdef(kinectin,protein,kinectin).
wdef(klc,protein,klc).
wdef(lamin,protein,lamin).
wdef(myosins,protein,myosins).
wdef(nmdar,protein, 'NMDAR').
wdef(nmdar2b, protein, 'NMDAR2B').
wdef(ntf,substance,'NH2-terminal fragment').
wdef(p70s6k, protein, p70s6k).
wdef(p78s6k, protein, p78s6k).
wdef(parp,protein, 'poly(ADP-ribose)polymerase').
wdef(pdk1, protein, 'PDK1').
wdef(peptides, protein, peptide).
wdef(pkb, protein, 'PKB').
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	206	979	-178	-352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	-255	97
	-76	-10390	-4298	-732	-1329	2508	-279	*	*											
13	1891	484	159	350	1092	-1	939	-607	452	-798	2975	440	751	-478	271	649	-518	125	545	2395
	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-53	-10402	-4831	-732	1329	-2638	-253	*	*											
14	-1544	117	99	-433	1201	-927	779	-558	-17	-318	-25	-1196	812	225	-301	-421	440	735	-2569	653
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	20	-10421	-6282	-732	-1329	-2245	-342	*	*											
15	-271	-1402	122	84	621	-135	786	-1396	-125	16	-836	-1064	657	-830	-798	-173	82	811	558	618
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-10502	-6072	-732	-1329	-3329	-151	*	*											
16	-1475	-1395	305	1025	1081	360	-400	-870	-768	-809	-3051	695	613	-548	-114	-1142	151	-98	1927	-111
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-41	-10494	-5199	-732	-1329	-3725	-113	*	*											
17	-945	24	278	129	1415	-574	164	-1466	-164	515	-238	833	463	-210	-2677	-785	-979	905	-25	-2438
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-118	-10455	-3687	-732	-1329	-3067	-183	*	*											
18	-903	83	828	842	1676	-1211	-1689	519	-65	-698	-2951	-483	349	886	-841	-1224	-1664	193	590	-247
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-58	-10373	-4702	-732	-1329	-3019	-190	*	*											
19	-604	-182	-2092	-158	1851	-1895	-84	840	856	-219	-2944	-188	607	-143	-763	-473	290	-2187	1413	114
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10365	-11365	-732	-1329	-2675	-246	*	*											
20	-946	873	129	-185	1399	-1954	-294	255	250	513	-1340	-2446	100	-1248	1200	-2351	775	-926	635	-188
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10435	-11435	-732	-1329	-2639	-252	*	*											
21	-985	-1396	77	-695	1037	-2004	-205	-216	636	647	-3052	1080	541	-171	-168	-2430	51	-405	-2630	1250
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-10495	-7334	-732	-1329	-2652	-250	*	*											
22	-2205	-1431	391	417	1650	-2038	1141	-697	-144	490	1149	-706	284	-2483	-2077	-1155	-661	295	282	1418
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-52	-10537	-4839	-732	-1329	-3319	-152	*	*											
23	190	-1396	119	-627	1701	-2003	-73	-2084	265	55	-112	-956	648	617	937	-2429	-320	-172	-2630	746
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10494	-11494	-732	-1329	-2740	-234	*	*											
24	-1493	461	222	960	1719	-1229	496	13	-767	524	-1910	-2576	-387	-194	758	-1633	-991	233	-2667	246
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10538	-11538	-732	-1329	-3374	-146	*	*											
25	-1957	599	-335	119	937	-389	-1832	-204	849	-272	-471	-332	235	-612	925	-1335	21	344	-2672	1054
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-29	-10545	-5725	-732	-1329	-3560	-128	*	*											
26	-472	134	-420	-549	1604	-2022	348	-454	826	46	-155	711	-224	874	16	-2448	-1125	-215	-2649	1130
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-38	-10517	-5292	-732	-1329	-2966	-198	*	*											
27	-499	-1408	982	-2739	1396	-2015	-48	-365	-347	493	1123	-2551	188	1109	384	-317	-2360	-1741	-2642	1604
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-75	-10508	-4318	-732	-1329	-2826	-219	*	*											
28	-2151	-1378	-417	288	1496	-1985	-15	-869	-693	624	-1250	699	483	408	440	-1438	-2330	-465	-2612	2022
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10472	-11472	-732	-1329	-2865	-213	*	*											

29	324	-1411	115	185	793	-2018	422	-1214	616	339	-3067	-1268	646	1078	-112	885	-599	-436	-2645	897
	206	979	178	352	36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	255	-97
	-56	10512	4750	732	-1329	-2887	-210	*	*											
30	-274	2097	1345	829	-597	-954	-1788	-963	-681	-469	-1882	-1739	700	790	678	-776	268	523	-2628	-2419
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-73	-10491	-4354	-732	-1329	-2901	-207	*	*											
31	-1182	222	623	536	461	-834	-1758	954	135	886	-3020	-887	-413	598	-2678	-1444	-2	-756	613	596
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-31	-10456	-5599	-732	-1329	-2527	-275	*	*											
32	1196	1488	1029	-163	-1851	-1234	-36	942	-1936	2	-3051	454	605	557	-870	-373	-271	373	-2629	810
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-60	-10493	-4638	-732	-1329	-2619	-256	*	*											
33	-934	478	634	-224	-756	-692	-1785	-479	-219	-175	443	725	1139	780	829	-1023	750	-851	-2625	-2467
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-69	-10489	-4442	-732	-1329	-2710	-239	*	*											
34	147	-1374	649	479	630	47	1225	27	49	-1018	4	-903	-935	147	330	-1376	916	-1204	-956	9
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-91	10467	-4043	-732	-1329	-2343	-317	*	*											
35	-2141	-1368	296	-86	1186	-30	-344	-919	-611	-13	-1005	-1858	478	760	406	-394	-21	-139	-2602	1782
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-73	-10461	-4366	-732	-1329	-2342	-317	*	*											
36	-677	600	1527	-213	476	-1985	65	294	-519	672	-3033	-1348	-953	882	-868	-2000	672	-311	-2611	608
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-32	-10473	-5578	-732	-1329	-2667	-247	*	*											
37	580	-1395	-438	-192	505	-604	185	45	-1156	979	-3050	-2538	-163	636	349	-1313	201	137	-2629	172
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	255	97
-	-47	10493	-4984	-732	-1329	-3697	-116	*	*											
38	-418	1347	739	-552	592	-203	-59	226	4	615	-3012	-1923	-86	862	245	-1556	-24	1123	247	130
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-2	-10447	-11447	-732	-1329	-3212	-165	*	*											
39	-873	2186	816	899	-809	-560	-353	-194	-967	-222	137	-2520	-529	1020	-423	280	-833	-447	-2610	1012
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10471	-11471	-732	-1329	-2695	-242	*	*											
40	-1805	-781	613	-935	1139	-801	1220	-497	-25	-2	-3074	-2562	850	641	-1550	-13	-562	-430	-2652	2131
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10521	-11521	-732	-1329	-2661	-248	*	*											
41	-381	1420	-492	-1975	-271	-1273	592	-86	263	96	354	-687	-561	636	266	-1199	875	256	-2689	1473
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
42	289	1850	131	-924	-1030	-2062	-283	-2479	47	905	-2917	-2599	509	1531	966	-1769	-6	-2446	-2689	991
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
43	-171	583	-660	-1238	-1172	-2062	-661	767	-1092	903	-3111	-1081	-277	1090	898	-1064	81	204	-2689	1310
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
44	-965	1662	-862	-152	-604	-627	414	-804	-869	383	-145	417	-2394	1951	265	-268	-1336	-113	-2689	1314
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
45	374	1081	-785	25	1187	-2062	-51	-3070	192	695	-3111	-572	-2394	1107	-930	338	-385	15	-2689	778
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

	1	-10565	-11565	-732	-1329	3499	-134	*	*										
46	565	304	673	360	1082	-969	-11	-471	-1427	1512	3111	-482	2394	602	87	1503	-2042	834	2689	825
	206	979	-178	-352	36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	12	-255	97
	-60	-10565	-4635	-732	-1329	-3499	-134	*	*											
47	418	21	-2564	-976	-1216	-187	-1800	-3020	-388	739	-1961	-243	-978	1516	-448	-2439	533	794	-2640	2302
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10506	-11506	-732	-1329	-3675	-118	*	*											
48	460	1406	160	95	2421	608	-1800	142	-202	858	-389	-2549	-2344	1727	-245	-443	-762	-660	171	-2482
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-24	10506	-5995	-732	-1329	-2459	-290	*	*											
49	-1271	-1437	1048	-1123	339	-813	346	50	-739	-33	-360	-2580	-2376	2048	579	-678	-550	205	-2671	1284
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10544	-11544	-732	-1329	-3002	-192	*	*											
50	666	746	-1057	-432	-2470	-1106	520	-575	335	764	-3111	-2599	-2394	966	422	-520	486	-357	-2689	1407
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
51	-708	1749	-381	-152	-2470	76	-1849	-785	411	105	-1257	-224	-23	1633	403	63	-325	-398	-2689	236
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
52	360	654	897	866	-2470	-412	276	184	-740	-831	-3111	62	385	248	-645	-1566	-966	1	1788	1039
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
53	629	737	922	-152	-883	-244	124	905	-1007	673	-640	-445	-504	301	-237	-221	-2408	-832	-2689	-716
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
54	430	893	-1901	-245	-106	-1397	-1849	1214	-1446	358	372	-1027	-771	420	-58	154	-81	188	-2689	872
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
55	-416	955	-950	532	446	463	818	-1782	535	498	-353	-626	-967	218	-1587	532	-1500	-812	-2689	1059
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
56	-250	933	-182	-129	-1635	971	173	139	-729	626	-1371	106	-216	-112	-25	274	-812	-1094	-2689	429
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
57	149	1050	501	692	-2470	806	592	-1124	-15	86	-1327	-1807	-224	-703	510	-532	-803	314	-2689	-84
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
58	561	-104	725	-133	-815	-931	1280	177	-45	851	-438	-1174	-527	-473	-5	-479	-2408	-1254	-2689	1305
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
59	989	973	67	-1693	947	-62	900	-397	-1003	-91	-2656	-948	199	1084	-2069	-783	-1677	-703	-2689	1800
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
60	-187	1718	336	922	-32	-1381	-24	-458	-328	689	-3111	-1774	796	-1113	-2769	202	-633	-162	-2689	783
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
61	235	1587	-177	-412	548	-222	1278	-3070	-1524	287	-3111	-1315	307	1431	-354	-67	-83	-452	-2689	583
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-89	-10565	-4081	-732	-1329	-3499	-134	*	*											
62	698	-1382	572	-74	-1677	476	732	-2996	-267	930	-304	-1352	-1319	-632	-1251	99	255	-1593	-2616	1295

	206	979	-178	352	-36	372	585	-635	438	-130	677	-164	41	-73	-335	54	27	-12	-255	-97
	-2	-10477	11477	732	1329	2200	-354	*	*											
63	203	1155	784	670	629	117	1036	-853	-966	996	-3111	-531	-619	816	-897	519	266	1159	2689	2531
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	335	-54	27	-12	-255	-97
	-50	-10565	-4917	-732	-1329	-3499	-134	*	*											
64	759	338	-522	609	2429	-687	1486	-1315	359	681	-3070	-1182	-987	-421	-2728	442	-156	44	-2648	672
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10516	11516	732	-1329	2608	-258	*	*											
65	974	-1455	84	183	-2470	-49	-163	-560	-446	773	-1767	-278	-416	421	-1832	207	-372	-141	-2689	435
-	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
66	869	73	53	-218	-883	-312	235	-385	-827	211	1454	-987	265	395	-1852	448	-1307	-1321	-2689	1346
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-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
67	530	-1409	906	696	346	-831	-1849	-132	333	810	235	-1312	-610	-128	-2069	-212	-458	-476	-2689	1162
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-50	-10565	-4899	-732	-1329	-3499	-134	*	*											
68	-335	-37	-2572	239	-823	-415	-1808	-811	-97	1312	361	-819	518	684	-533	-97	-2367	174	-2648	857
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10516	-11516	-732	-1329	-2598	-260	*	*											
69	629	-1455	-581	-370	261	622	328	-1326	-1996	749	-321	-356	172	-252	-192	174	-471	411	-2689	-1079
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
70	1036	647	514	-121	-314	483	-1849	-375	12	32	-3111	-2599	79	-1	-1033	262	-1491	-904	-2689	1300
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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71	1010	368	337	-829	1366	-542	1849	-42	444	-163	121	-2599	-673	744	-1209	-7	-609	-2446	-2689	1085
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	11565	-732	-1329	-3499	-134	*	*											
72	182	179	862	536	-58	187	592	310	609	824	-3111	-2599	-817	-1270	-1209	-1332	-1464	-201	-2689	450
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
73	192	-816	663	827	-803	-25	-1849	-1015	-59	767	-2917	-1344	-1350	1458	-1952	-1280	-1433	681	-2689	1025
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-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
74	113	-752	832	-1098	-1045	-684	-101	-870	-1003	1356	-428	-356	-57	905	-1262	-358	-1464	-57	-2689	952
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
75	297	1131	465	-474	-602	274	479	-606	-550	-146	-3111	-1032	851	1288	511	-395	-1464	-346	-2689	56
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-45	-10565	-5063	-732	-1329	-3499	-134	*	*											
76	110	-1418	102	1055	-2434	-1360	93	-413	827	6	-652	-862	958	-846	628	-920	-287	-1172	-2652	1119
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-76	-10521	-4296	-732	-1329	-2666	-247	*	*											
77	-2167	-806	991	605	639	186	964	-3009	249	166	-1593	-701	-1510	1126	-696	-549	-41	-864	-2628	1470
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-66	-10492	-4511	-732	-1329	-3690	-116	*	*											
78	-1127	-1340	437	-2672	278	668	454	-80	220	-118	-2996	-2484	-189	724	205	73	133	675	-1234	640
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-34	-10428	-5483	-732	-1329	3836	-105	*	*											

79	-414	490	839	635	-336	914	266	-1919	202	-142	188	-2457	1287	-464	-2628	-2347	-71	-40	246	171
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-	-39	-10395	5261	732	-1329	-2683	-244	*	*											
80	-566	-1287	946	678	229	-196	1535	-1964	20	-1494	40	574	525	768	-1489	-1134	-326	-93	-2572	1056
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-55	-10425	-4757	-732	-1329	-3840	-104	*	*											
81	-904	-1294	925	353	-884	-322	875	188	883	262	-565	187	811	-640	-874	-1066	-2217	389	-2528	789
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-62	-10370	-4599	-732	-1329	-3942	-97	*	*											
82	488	1244	748	1210	-2260	-1143	862	-2859	122	-357	-2900	747	361	-1079	-804	-135	-117	-222	683	323
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10310	-11310	-732	-1329	-2728	-236	*	*											
83	-1102	-1307	-1216	870	-740	701	94	515	285	-628	-433	-2451	310	1477	-831	-343	-972	-56	-2541	1048
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-89	10387	-4083	-732	-1329	-3914	-99	*	*											
84	-2009	141	-386	1064	98	-526	1401	-1748	-78	-559	920	311	-2174	414	-608	441	658	329	636	-1264
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-	-49	10299	-4953	732	-1329	-3267	-158	*	*											
85	2004	600	289	-77	-2246	-626	1465	-53	602	377	522	-706	501	-270	-210	-681	-880	273	859	1256
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-47	10293	-5004	-732	-1329	-4051	-90	*	*											
86	-680	404	681	-1141	229	-1075	1396	-432	763	413	-2850	-882	153	-2246	-356	-141	469	-130	-2428	1155
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-25	-10248	-5947	-732	-1329	-3438	-140	*	*											
87	993	-1205	729	554	260	-85	-1599	-335	1342	-1161	-181	-46	-52	-443	545	367	-1510	303	168	829
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-	-39	-10262	5259	-732	-1329	-2756	-231	*	*											
88	1434	-1245	-306	43	-1452	-780	335	-1199	393	368	-12	-351	171	291	271	123	39	1060	626	28
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	97
-	-73	-10311	-4368	-732	-1329	-1620	-568	*	*											
89	396	698	136	205	835	-1181	456	-56	-717	-395	-1239	-237	-632	751	-2692	-255	-1360	867	858	1237
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-	2	-10473	-11473	-732	-1329	-2627	-255	*	*											
90	1770	1423	-105	542	813	518	-399	-1460	-23	921	-774	-28	138	675	-333	-1345	-740	-265	239	237
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-46	-10527	-5025	-732	-1329	-3070	-183	*	*											
91	-2000	651	-173	697	558	-678	769	-648	-692	368	90	683	906	639	-814	-393	-699	-36	468	-954
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-39	-10504	-5276	-732	-1329	-2902	-207	*	*											
92	-288	-1401	-73	773	-816	-1086	159	-241	1958	55	-3056	-1098	-540	-380	185	-867	-916	-2392	875	989
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10500	-11500	-732	-1329	-2810	-222	*	*											
93	-885	-1433	-1831	318	-845	-1596	887	-60	926	-65	199	-661	598	858	1238	-804	-268	-1158	1739	-86
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-105	-10539	-3850	-732	-1329	-2445	-293	*	*											
94	-279	56	408	990	1553	-741	-687	-1509	750	-526	598	507	-302	-1042	521	-938	-1081	-211	-2630	259
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-	-52	-10495	-4840	-732	-1329	-3031	-188	*	*											
95	232	1257	-690	477	1494	-1985	1307	-997	53	382	1300	-881	-1297	710	794	-2411	-1073	-990	-2612	-967
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-	2	10473	-11473	732	-1329	3753	-111	*	*										
96	277	74	1024	194	793	937	1019	96	-409	274	3034	-1327	1332	1059	463	255	638	251	2087	1264
	206	979	-178	352	36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	12	255	97
	-31	10473	-5614	-732	-1329	2550	-270	*	*											
97	838	1406	-2563	885	-771	1086	852	112	1405	21	1114	-563	527	69	1513	1604	-212	248	257	175
-	206	979	-178	-352	-36	372	585	-635	438	-130	677	-164	41	-73	-335	-54	27	-12	255	97
-	-31	-10506	-5602	-732	-1329	-3088	-181	*	*											
98	-1658	-1401	-501	417	-2416	1771	533	-445	1330	-932	640	-1480	890	723	-1328	1153	-271	282	-2635	283
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	335	-54	27	-12	-255	-97
	44	-10500	-5097	-732	-1329	-3694	-116	*	*											
99	182	89	-656	486	120	-1537	-1760	-717	724	431	943	193	156	-416	149	-49	-1067	264	-53	-1237
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	101	-10459	-3903	-732	-1329	-2339	-318	*	*											
100	860	486	-563	-33	-2372	-1964	108	-451	118	648	-1225	-2500	-259	1173	547	-610	-365	20	-555	556
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-13	-10448	-6913	-732	-1329	-3442	-139	*	*											
101	-626	-1359	1056	988	-399	-441	798	-1131	513	-315	1885	-1702	-2298	-2411	-623	-1120	828	-1220	1050	934
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-76	-10451	-4314	-732	-1329	-2299	-328	*	*											
102	-1382	212	829	-951	-918	-1446	161	-755	127	1027	476	-528	-954	-386	760	853	-345	-2340	10	769
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	-154	10470	-3316	-732	-1329	-3579	-126	*	*											
103	-828	-1256	241	1342	-2271	-1044	1495	-276	1462	-474	816	-2399	50	54	-881	473	-2208	-1178	620	-1330
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-110	-10326	-3785	-732	-1329	-3153	-172	*	*											
104	-948	-1207	420	902	272	-617	681	-1361	536	20	1242	-2350	-2145	458	-38	683	503	1040	2441	898
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-77	-10266	-4295	-732	-1329	-1765	-503	*	*											
105	150	-1333	375	292	-140	-1286	-1727	336	606	175	486	-2476	-390	-108	656	-1356	138	466	594	359
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10420	-11420	-732	-1329	-2307	-326	*	*											
106	202	-1412	-602	540	-559	-274	370	455	1648	-1957	960	-1014	-373	631	73	-54	-1038	-310	-405	-961
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-	-85	-10515	-4148	-732	-1329	-2251	-340	*	*											
107	1220	-1410	-1277	342	-1124	-597	-47	-218	1058	387	-177	-1318	-1678	-185	-444	-759	-1077	367	-2644	673
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-10512	-7673	-732	-1329	-1782	-496	*	*											
108	33	1209	-226	1207	-770	-894	-1905	-1576	1601	-705	393	-1202	-761	-669	65	458	-641	-431	-2744	-463
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-10633	-7858	-732	-1329	-1912	-446	*	*											
109	144	-1567	-588	1058	-453	-2175	-1962	-350	1423	-283	1484	-306	-529	223	-130	-579	519	-2559	-182	-166
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10700	-11700	-732	-1329	-2413	-300	*	*											
110	-873	-1589	111	1208	-345	-2196	337	-59	862	385	272	-2733	-369	1261	-100	-642	-147	-593	343	-1178
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-	-60	-10725	-4642	-732	-1329	-2460	-289	*	*											
111	-7	-1555	-249	760	-602	-729	1103	-1438	-48	818	-1413	-543	-755	1309	774	-711	-126	-1520	-503	-524
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10685	-11685	-732	-1329	-2294	-329	*	*											
112	1	353	-681	857	-605	-507	938	704	838	27	372	-614	-762	24	-112	-1229	-219	-938	97	213

-	206	979	-178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-8	-10717	-7679	732	1329	2189	357	*	*											
113	328	-1603	155	945	131	2211	1823	-3218	1137	430	1132	-2747	-1277	992	476	2637	151	943	943	-82
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10742	-11742	-732	1329	-2907	-206	*	*											
114	-220	-1603	-342	854	-2619	-2211	50	896	1174	955	-1078	-967	-2542	659	154	-1186	-2556	-1081	1162	426
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10742	-11742	-732	-1329	-2907	-206	*	*											
115	-897	-1603	-34	315	-2619	-33	387	304	-534	330	634	-1046	-313	1474	1198	-988	-419	28	-2838	431
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-	-1	-10742	-11742	-732	-1329	-2907	-206	*	*											
116	533	-1603	-2761	-349	-642	-1040	504	828	841	-353	668	-436	-1023	1568	-528	-579	-2473	750	-2838	116
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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117	395	-1603	-1193	302	-2001	-1518	1399	-3218	47	375	-540	-589	-2083	1032	-81	182	1507	-1224	-887	430
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10742	-11742	-732	-1329	-2907	-206	*	*											
118	-729	-1603	305	362	1446	-620	165	284	441	-940	493	-26	-673	-321	-1205	323	-742	-270	569	945
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10742	-11742	-732	-1329	-1482	-639	*	*											
119	927	-1663	-298	-1529	-491	-383	2047	-3278	165	410	-786	-717	-349	440	974	-1113	-442	-1020	-2336	1109
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10811	-11811	-732	-1329	-2546	-271	*	*											
120	273	-1663	-2821	256	-1016	-461	2784	-712	-584	-264	-3319	-114	-855	1542	669	275	-1010	-2655	850	-404
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10811	-11811	-732	-1329	-2546	-271	*	*											
121	257	780	-899	263	1085	-20	617	-3278	396	-1559	1380	-122	-2602	753	51	645	328	1111	2897	618
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
	1	-10811	-11811	-732	-1329	-2546	-271	*	*											
122	710	-1663	-323	344	850	-37	678	-977	369	-1517	1128	759	-978	-43	76	-737	-1135	-494	-2897	1124
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10811	-11811	-732	-1329	-2312	-324	*	*											
123	-69	-1617	-274	347	376	444	-520	-988	172	38	430	751	-696	-861	-1187	52	-1320	291	1510	589
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	1	10818	-11818	-732	-1329	-2494	-282	*	*											
124	27	86	-842	-487	2684	1011	-2063	-997	717	179	471	-317	386	4	881	-969	-317	186	-2903	-620
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10818	-11818	-732	-1329	-2494	-282	*	*											
125	-446	-1669	-221	-450	-1211	-788	-2063	-114	504	596	-1207	1310	-644	1906	-2862	-118	-206	-523	-2903	-54
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10818	-11818	-732	-1329	-2494	-282	*	*											
126	-605	-1669	-1140	358	339	-1117	-2063	-3283	-451	856	1623	-101	-130	776	492	511	522	-2032	-2903	-167
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10818	-11818	-732	-1329	-2494	-282	*	*											
127	-514	-1669	-194	1415	571	-636	590	-1385	63	-963	223	-522	79	895	-870	-86	877	-1234	-2903	298
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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128	987	-1669	-402	1097	530	-182	725	-207	57	202	-639	-529	-1135	-1083	-892	55	-302	-1041	-2903	-434
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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129	664	-1669	-720	1308	180	580	305	432	280	-243	3324	-1438	-2607	617	1240	9	127	372	2903	366
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-	1	10818	-11818	-732	-1329	2494	-282	*	*											
130	350	91	-163	1527	980	-878	-2063	444	-62	527	-3324	-130	-1348	-755	115	443	-798	-558	2903	1252
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-	42	10818	-5152	-732	-1329	-490	-1797	*	*											
131	806	1954	578	1252	787	2345	-548	-354	370	715	-1037	-1930	-2676	-1526	-677	-902	-1262	-795	-2972	-737
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10898	-11898	-732	1329	-1885	-456	*	*											
132	2511	242	-340	897	1368	-1082	-82	-600	1746	809	-1457	-322	-1156	220	-2150	-2128	-680	-1327	-2972	397
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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133	44	-622	-2895	75	1276	-1417	276	-87	736	1235	1131	-443	-2676	291	-854	-2771	-2690	379	138	-389
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-10898	-6381	-732	-1329	-1885	-456	*	*											
134	1508	954	-1449	1202	1507	-583	62	-3337	13	146	525	712	-2662	640	393	-2756	-970	-288	-2957	1327
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	1	10881	11881	-732	1329	-1497	-631	*	*											
135	768	93	1070	308	1053	-28	-2132	406	437	-130	48	1027	-1307	-127	-761	-369	-893	-72	-2972	1379
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-	-1	-10898	-11898	-732	1329	-1885	-456	*	*											
136	751	1738	-215	460	-267	-275	-2132	1586	834	-154	379	-494	-552	-709	-1650	-2771	-365	-75	-2972	-576
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	22	-10898	-6073	-732	-1329	-1885	-456	*	*											
137	1306	-660	147	790	-1064	-245	-38	173	1159	321	-3375	-1703	-1685	831	1213	-1499	-327	-484	155	473
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	97
-	103	-10877	-3870	-732	-1329	-1428	-670	*	*											
138	809	-342	-2808	-1735	-2666	-476	-2045	37	1288	408	131	422	-2589	-213	-473	-460	616	343	-2885	558
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-57	-10797	-4721	-732	-1329	-2669	-247	*	*											
139	-707	-474	-364	-177	-367	-226	-1997	-542	137	1623	-490	-561	-1313	-1590	-60	-703	-805	-1083	2673	257
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-19	-10742	-6321	-732	-1329	-1084	-921	*	*											
140	2101	564	723	-1104	-1455	719	623	-3293	-348	204	-565	18	-1644	1142	-493	1244	-1869	168	-1219	634
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10830	-11830	-732	-1329	-1852	-468	*	*											
141	-86	1098	-2263	-1342	139	336	766	-129	-432	132	2121	-746	1295	-1864	-2449	250	-1008	350	585	-128
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-10850	-5356	-732	-1329	-1793	-491	*	*											
142	-338	980	341	-859	-215	-528	115	-950	-574	983	-242	-1844	-35	-2037	-780	-1193	-686	889	-101	1946
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-26	-10832	-5827	-732	-1329	-1995	-417	*	*											
143	-1925	369	-89	-1743	-511	1227	424	-30	673	-1039	230	-1010	1271	-2723	-454	-976	-1440	579	-2905	1705
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144	633	-45	-279	383	129	-532	-387	-1879	-277	-190	-999	-1552	-2573	-1064	731	-739	-955	1297	1135	1387
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-	-1	-10779	-11779	-732	-1329	-2208	-352	*	*											
145	-1887	-1650	1103	-400	1642	1058	1656	-832	-50	-691	-3306	-2794	-549	-2703	-338	-645	-2603	498	1007	953
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	23	-10797	-6034	-732	1329	-2680	-245	*	*										
146	1011	-1632	964	145	2064	1658	1192	-1421	-1431	1047	-974	250	-2570	1051	-237	2665	-1271	74	236	1166
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	-255	-97
-	150	-10776	-3352	-732	-1329	2803	-223	*	*											
147	-62	-742	-303	-1076	451	-97	2730	562	838	293	-1917	188	-2443	-2557	-930	-1002	1011	214	607	-1574
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-	-79	-10627	-4245	732	-1329	-3404	-143	*	*											
148	-749	747	378	-154	-153	-361	2948	-73	555	-1142	-1725	-1603	-2378	-524	-2753	226	861	-21	-2673	-22
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-48	-10549	-4965	-732	1329	-3638	-121	*	*											
149	1279	-1400	-351	-21	201	908	1477	-1699	784	-337	-3056	-1161	-1627	-2452	-1799	90	-699	-2391	255	1207
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-	-38	-10503	-5293	-732	-1329	-3104	-178	*	*											
150	-275	-1392	3	-912	1586	-1999	581	-252	1403	-1793	-3047	278	-800	-604	630	194	-1081	802	-2626	-600
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-75	-10493	-4332	-732	1329	-3774	-110	*	*											
151	-915	-1331	1827	-417	-34	334	326	983	26	-501	-2987	-358	-2270	-773	-433	-333	-588	418	-2565	-168
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	55	-10420	-4770	-732	-1329	-3928	-98	*	*											
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	-71	-10366	-4399	-732	-1329	-4024	-92	*	*											
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DATE Mon Mar  8 11:42:18 1999
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NULT       -4  -8455
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HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

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         -3892      *   -101
     1     796    224   -933  -1107   -791    345   -170  -1390    370   -229  -1432    404   1515   -828  -1090    -39   -728   -767   1428    633
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     -      -9  -7945  -8945   -732  -1329  -3457   -138  -3892      *
     2     256    153  -1005   -458    443    771   -242  -1462   -389   -957  -1503   -991    148   -900  -1162    685   1250   -543  -1081   1305
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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	34	-940	1858	-619	-783	2315	-774	585	-1781	695	212	-1822	-136	-1105	185	-847	-145	-186	-1158	-1401	135
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	-	-6	-8510	-9510	-732	-1329	-2398	-303	*	*										
	35	-214	2202	-1381	-1115	512	-452	746	-1838	-47	374	-213	-925	-77	-333	749	326	295	-662	-1457	655
	-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-	-6	-8617	-9617	-732	-1329	-2913	-205	*	*										
	36	-311	2007	-992	-868	-108	28	1013	-650	67	690	597	-1367	-137	512	-1537	175	-351	116	-1457	7
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	-	-6	-8617	-9617	-732	-1329	-2913	-205	*	*										
	37	-394	1506	-921	-1555	640	887	-617	-1838	-34	-263	-1879	-1367	792	779	-641	564	620	-27	-1457	-1299
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	-	-6	-8617	-9617	-732	-1329	-2913	-205	*	*										
	38	1004	2135	-1381	-1555	1697	140	-617	-1838	-122	359	-1879	-1367	-259	576	-1537	-1257	379	-272	-1457	-1299
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	39	166	1147	-1381	-1555	-423	-830	-617	-1529	711	1113	-1879	78	108	1287	-1537	-535	337	-1031	1225	-292

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-	-6	-8617	-9617	-732	-1329	-2913	-205	*	*											
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43	-101	1922	-1381	-1555	423	-830	-617	-1838	-765	-351	116	-1367	14	-1275	-196	184	2009	697	-1457	-1299
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45	-502	1983	-1311	-283	-1168	-760	-547	-1768	1501	161	-1809	-634	-89	1109	-1467	205	-73	226	-1387	176
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49	-963	3110	-1348	-1521	-1205	-797	-584	-1805	954	-642	-1846	-614	438	-398	-1504	598	832	-205	1484	744
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-	-69	-8270	-4528	-732	-1329	-3485	-135	*	*											

54	-315	1857	-385	-923	-1038	-630	-417	-1637	-564	1160	827	550	323	679	-1337	25	-339	-834	1278	-1099
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64	-195	2183	-989	-1163	-846	-438	-225	-998	1707	-657	-1487	-975	-770	-883	-1145	-864	160	1473	681	-907
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65	-605	1556	-989	-1163	-846	-235	-225	-1446	66	-488	-1487	746	893	901	-1145	-273	1536	-94	404	-907
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66	-101	3140	-363	-1149	-833	-425	-212	-1432	-359	143	-1473	-961	292	-870	-1132	508	-195	1020	-1052	-894
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67	-565	1100	-949	-1123	-807	-399	-186	-1406	-333	-690	-1447	-935	1798	-844	-838	-239	936	95	2283	1279
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68	-440	333	-825	-998	-682	-274	-61	-778	-208	514	-1323	-810	24	1	-199	-372	-129	1847	-901	-743
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-	-103	-7341	-3997	-732	-1329	-4148	-84	*	*													
69	-410	364	448	-564	159	-243	-30	-431	-178	-182	-1292	-780	-575	1998	903	-178	-360	-628	-870	-712		
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70	-403	370	-788	-961	-645	-237	-24	869	287	1016	-655	-774	-569	118	-944	561	-583	79	-864	-706		
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71	-379	394	-764	-937	-621	-213	0	-392	-7	-583	-1262	-749	-544	-658	-70	700	823	115	3347	-682		
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72	-314	459	-699	-872	-556	-148	65	-1155	378	-503	-1197	-684	-480	-593	-855	942	-494	1818	-775	-617		
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97		
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73	-180	593	1278	-305	-422	-14	199	-1021	52	-516	-1063	-36	-345	-459	-444	879	-160	146	-641	-483		
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74	381	644	-514	-688	-372	36	249	-971	102	-466	-1012	-500	-295	-408	-670	1646	-97	-348	-590	-432		
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-	-170	-6305	-3348	-732	-1329	-4604	-61	*	*													
75	-76	697	-460	-634	-318	90	303	-917	156	-412	-958	-446	-241	-355	-617	-336	1973	-294	-537	-378		
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ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
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DATE  Mon Mar  8 11:42:34 1999
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y
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         -2810      *   -222
      1     24   -736    758   -258  -1752   1483   1437  -2351  -1278  -1846  -2392   -275    415  -1789  -2051    321  -1689   -541   2589   1402
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      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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      9  -1279   -976   -584   -804   -979    554   3173   -679   2055   -739  -1932   -209   -839   -974  -1308   -107  -2906  -2945    429  -1366
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      -    -27  -1142  -5808   -732  -1329  -3144   -173      *      *
     10     15   1116   -698   -560  -2969    424   3235  -3568  -2495  -1410  -3610   1903    218    354  -1308   -797  -2906  -1944   1933    242
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      -     -1  -1142  -2142   -732  -1329  -3464   -137      *      *
     11  -1218    735   -822    347  -2975   1567   1089  -3574   -789   -248  -3615   2528  -1159  -1318  -3274  -1329  -2277   -579   1931   -950
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26	-1465	-2137	535	1501	-3152	-78	-1552	-353	-1080	-1199	-1353	859	257	1359	1466	-233	-555	-1636	-3371	-3213
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27	-2931	-2157	621	-2753	-3173	-2765	752	906	258	-816	-3813	83	544	2194	2245	-465	-2466	-1666	-3391	-408
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38	1505	-2110	-167	-2715	-3125	-503	946	-570	1114	-350	-3766	-1874	-1234	351	-186	-496	7	336	-3344	997					
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39	-469	-2110	97	-2715	-2266	-841	2180	-2815	1977	-138	-3766	-543	-391	35	38	342	1457	1253	3344	1677					
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61	-2872	59	378	514	334	852	1011	1859	-2144	-1042	-1300	643	-3037	-1140	1746	-1717	781	186	982	-2101					
-	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97					
-	-65	-11304	4508	732	-1329	-1487	-636	*	*																
62	-1775	87	656	-1407	313	-456	517	2077	-2138	-137	-152	1444	-3026	-24	-1448	-1693	-636	1110	726	-862					
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97					
-	-1	-11291	12291	732	-1329	-2683	-244	*	*																
63	-2866	-2093	1437	-2214	-316	-828	579	-107	306	1116	-160	2516	-3031	-2257	-23	-415	-59	-812	-1291	-578					
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-	-86	-11297	4116	732	-1329	-2052	-398	*	*																
64	-860	-2022	1321	-3353	-1003	-830	641	-3637	-405	-373	-3678	3282	-2961	-180	-1333	-3055	363	666	-3256	-743					
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-	-26	-11215	5817	732	-1329	-2531	-274	*	*																

65	2795	-42	1598	3353	-3037	1640	1069	-1520	-1225	-2341	-454	2722	90	-3074	1333	1370	1101	92	3256	3098
	206	979	178	352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	12	-255	97
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66	-1450	-1968	-3126	-427	792	2220	2779	-516	-44	-3078	3624	-255	-1103	298	-418	-1615	-459	-667	-3202	3044
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-28	-11152	-5713	-732	1329	-1493	-633	*	*											
67	-38	-2062	-444	3393	644	-142	3521	-1577	-854	-646	-3718	-246	-1561	-381	-2026	1115	-928	205	-3296	-750
	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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68	1258	446	487	-1643	2102	-669	847	-2799	-517	-2388	-2077	-1242	-2318	273	-3400	-62	1060	522	-3320	-3161
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-24	-11288	-5934	-732	-1329	-2274	-334	*	*											
69	-952	-1117	1413	-371	2574	-1314	1041	704	-1311	-856	-174	775	-506	-548	83	-967	-507	157	315	-838
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-24	-11288	-5934	-732	-1329	-1854	-467	*	*											
70	-1435	2108	233	-569	-1130	-837	-324	-125	-669	-1749	1011	2132	-1307	1173	-2582	133	-1464	1591	-1312	-3184
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-47	11314	-4986	-732	-1329	-1898	-451	*	*											
71	-1361	107	348	607	-1336	415	-292	-433	-1101	-519	-840	694	-3029	-170	-1428	-828	-993	2009	313	8
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-72	-11294	-4363	-732	-1329	-2786	-226	*	*											
72	-2790	-1074	11	1631	2312	1164	-2411	-204	-2558	-212	-2044	-680	-536	-523	-858	-1364	-71	-2446	-3251	-1478
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	-53	-11208	-4802	-732	-1329	-2476	-286	*	*											
73	-1473	1990	1066	128	2432	25	-2384	-2736	453	-75	-3646	-719	343	-940	-1988	23	-535	-2425	980	318
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-55	-11177	4749	-732	-1329	-2145	-370	*	*											
74	-803	-1990	2823	-1091	-792	334	-2384	-3604	-999	372	-392	-136	-725	-3042	-1988	-565	691	-2981	-3224	-684
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75	-575	-1997	2291	-2167	-2188	83	-1457	-3611	-264	-673	-3652	810	639	-3049	-1529	1227	-184	-1435	-3231	429
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76	-700	-1904	1671	2010	-676	-735	847	-1473	-570	-470	-3560	-295	-370	660	-1284	1836	-1020	-551	-3138	143
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-309	-11086	2378	-732	-1329	-2875	-211	*	*											
77	-238	-639	1365	-1363	-2698	30	-1036	-1343	84	-455	-549	330	-284	2715	-1440	111	-862	-2674	-2917	-2759
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	-220	-10835	-2828	-732	-1329	-2628	-255	*	*											
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79	480	-1846	-484	-2419	-2861	133	811	-2513	1916	-2956	-1769	-292	-187	232	-50	916	-2134	-691	-3080	1621
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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80	1593	-1989	3147	-2590	-218	-250	-2383	-1114	-1234	-399	1046	-472	-138	-207	-552	-139	-900	1374	-3223	1106
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	-8	-11182	-7685	-732	-1329	-918	-1087	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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	206	979	-178	352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	-255	-97					
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90	-1862	-2080	-1410	-2213	-286	-631	591	-3695	-2622	-236	-3736	-434	-352	556	646	-87	1709	-70	-3314	2670					
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91	1071	110	-1413	-1643	814	-2693	703	-3700	-1097	-619	-966	-3229	-550	379	1779	-494	-587	463	-3320	2866					
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92	-2064	-2086	1738	22	989	-1459	1826	-2248	30	1234	-552	-3229	-1274	22	1955	-967	83	-3077	-3320	-38					
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97					
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93	138	-2086	-1413	-3417	1392	-1459	1773	-81	42	1354	-3741	-1242	-814	546	506	-757	-2409	-208	315	-838					
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94	-589	-2001	-1048	-2169	-966	-1339	2360	1771	-56	-1173	-562	-3144	-987	2339	-1051	-99	-1590	-595	1398	-1467					
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95	-1978	-1961	-1221	-117	2257	68	1836	-628	-807	18	-2015	-812	-712	2477	-1972	-1492	-2914	-2953	523	-389					
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97					
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96	-2330	-494	-3147	-3321	2520	-201	3393	-1030	-375	-1067	-144	-1092	-2928	-29	-1988	516	-899	-575	1266	-3066					
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97	-2790	-2017	-861	159	1900	36	3775	-167	-1210	-916	-3673	-1823	-2955	-523	-674	-381	-1333	-403	433	-3093					
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98	-1511	-1074	-1305	-620	2875	-1359	3562	-3631	-1210	-916	-3673	-1133	-2955	-3069	-1316	-468	-577	-3008	1832	117					
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97					
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99	-2785	-2012	-515	-755	-524	-331	3902	-3626	-2553	-1027	-3668	-319	-2950	-3064	-1313	108	-85	-3003	4121	-3088					
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97					

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100	2733	-1960	350	1479	533	1854	2036	-3574	-2501	-1840	-1986	-1206	2698	-924	1259	-665	1268	675	4393	3035						
	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	335	-54	27	12	-255	-97						
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101	-441	-1921	353	-3253	-728	2066	1034	-3536	523	-1726	-3577	-71	166	-2973	-2430	1332	-471	-2913	1628	-2997						
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97						
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102	-561	272	-1041	-562	-2993	770	157	-1487	61	-978	-422	-218	-378	-487	-640	2138	149	-1442	-3212	-711						
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103	-612	267	1821	574	-3018	-174	128	-1532	-1016	1127	-3659	10	-274	-1637	-3317	218	-146	-1253	-3237	91						
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	-141	-11183	-3433	-732	-1329	-2172	-362	*	*																	
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97						
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109	-1021	-2135	-704	1578	-1166	26	329	-1684	-1378	-483	35	451	-3074	-1161	-3449	2062	761	143	3369	3211						
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110	-882	-2135	167	2254	-3150	-426	3417	-3750	-248	-3244	292	-1312	-3074	-887	-3449	-349	-889	207	-3369	-3211						
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97						
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97						
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115	-411	-2113	-1265	617	-1737	1010	757	-3728	2148	-1166	-278	185	-1310	-3165	-1582	-860	-1993	517	-3347	946						
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97						
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	-48	-11294	-4945	-732	1329	-2199	354	*	*																	

117	137	-2067	-3225	33	59	-1049	1802	-444	1898	-979	516	-1209	-3006	-3119	428	-3100	-1630	-774	-3301	2631				
	206	979	-178	352	36	372	585	635	438	-130	-677	-164	41	-73	335	54	27	12	255	97				
	-25	-11267	-5891	732	-1329	-1882	456	*	*															
118	500	-2091	-1108	-374	971	-1006	1935	866	-179	-535	554	-3234	-324	-3143	-433	288	-3043	702	-3325	2834				
	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	335	-54	27	-12	-255	97				
	-24	-11294	-5937	-732	1329	-2384	-307	*	*															
119	2177	-1114	-1135	-978	735	-200	1009	-2248	-2613	-445	30	-1212	926	-3124	-3386	-915	-1477	184	-3306	650				
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97				
	-1	-11272	-12272	732	1329	-2221	-348	*	*															
120	1402	-2096	-3253	1708	1102	-676	1447	-423	-1105	65	603	-3239	514	-3148	-3410	-1186	-695	149	311	-843				
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97				
	-1	-11299	-12299	-732	-1329	-2696	-242	*	*															
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	24	11299	5939	732	1329	-2696	-242	*	*															
123	-404	-2072	-599	3403	-3087	-1432	3757	-209	-174	1038	62	-955	-3011	85	-1395	-1934	-658	51	1143	-3148				
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	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	-12	255	97				
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127	-198	-2002	1379	-2160	445	-1152	-171	-3616	765	-1620	-234	2156	-385	571	-1058	-981	-1317	-2428	3955	428				
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97				
	-30	-11192	-5616	-732	-1329	-2858	-214	*	*															
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	-455	-10982	-1890	-732	-1329	-989	-1011	*	*															
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131	285	-1975	527	-951	-901	-14	-2369	-3589	2217	-993	-3631	-1215	-413	-3027	-469	-1523	-1565	-2966	-3209	2768				
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	-41	-11161	-5182	-732	-1329	-2928	-203	*	*															
132	-750	-1942	488	-524	18	1173	-2336	-840	-2483	-361	-3597	97	-1118	-2994	-1222	788	-1869	-153	-3176	2756				
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97				
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-	-8	11109	7682	732	-1329	-2663	248	*	*											
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-	-64	-11170	-4543	-732	-1329	-2534	-274	*	*											
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-	-1	-11256	-12256	-732	-1329	-2581	-264	*	*											
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-	-1	-11268	-12268	-732	-1329	-2260	-338	*	*											
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142	-1082	-2089	2039	-497	-3104	1053	-1505	-306	-465	-1292	-3745	-1458	2107	-2251	-1181	-1697	-1455	489	3323	-866
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143	-160	-2082	2008	-2692	-3097	2000	-525	104	-2139	-899	-3738	347	-508	-825	-747	-1947	733	228	1294	3158
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144	231	640	1482	-2737	-3150	2109	-2529	419	-205	1185	-3791	-3278	-1343	-507	-92	-1509	-761	-519	-3369	-3211
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	25	-11281	5912	-732	-1329	-1517	-620	*	*											
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147	459	-2140	1485	-990	184	-567	-82	989	-708	451	-3796	-1315	-3079	-353	-3454	-1744	-2455	2413	-3374	-2154
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149	24	-2118	3276	-1683	150	2123	-2512	1427	-1532	-153	547	-478	-3057	199	-3432	-1067	-3071	762	-3352	-1537
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150	-171	-2140	-3298	-447	2074	460	-2534	2232	-1381	-102	-2115	-3284	-1346	5	-1498	-3173	-764	525	-3374	-3216
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-	-23	-11350	-6024	-732	-1329	-2468	-288	*	*											
151	542	-1145	-169	194	2539	-1671	-2512	-674	-1350	1250	1947	-1282	-772	199	-3432	-3152	-730	-696	-3352	-3194
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	-65	-11325	-4503	-732	1329	-2006	413	*	*																
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	206	979	-178	352	36	372	585	-635	438	-130	677	-164	41	-73	335	-54	27	12	255	97					
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153	-1314	-2017	-2445	190	532	-757	-178	588	1897	-519	-435	-674	108	554	-1274	-3050	-1101	1500	-3251	-554					
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97					
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154	-612	-2113	-736	436	-640	1370	-2507	-624	-442	-511	-3769	38	64	-782	-1462	-244	-1226	1855	-3347	-1530					
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	154	-11320	-3312	-732	1329	-2683	-244	*	*																
155	61	-1979	96	-257	678	2115	-2373	-1535	-128	-1845	-3635	850	475	110	-3293	-179	-2290	-1149	-3213	144					
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157	1740	-2071	-385	420	-3087	-2679	601	-1627	999	-141	-3727	-590	1019	-596	-739	68	-170	-2472	-3306	-853					
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158	-340	-2016	713	358	-400	-1207	-415	-3630	1990	-798	-1963	1729	-555	-266	-983	-76	-746	-734	-3250	-3092					
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159	-1022	-1854	594	-588	-2869	-803	616	81	-357	-707	-459	1903	1871	384	-3168	-1629	-583	441	-3088	-847					
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160	671	-2092	-1420	375	-2256	61	-2487	-370	868	-182	-3748	404	2372	-242	-2573	-1620	-1373	-575	308	984					
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163	-824	-2096	-316	172	-1225	-809	-2490	508	1770	-304	-3751	65	-1033	2422	-1670	-906	-1437	-1571	311	5					
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164	181	-2118	75	-759	-344	-843	-330	330	1941	-895	65	-1500	811	-318	-1128	-1485	-1082	1082	-3352	-3194					
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97					
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-	-25	-11272	5893	-732	-1329	2221	-348	*	*											
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-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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	-404	-10139	-2039	732	-1329	-4382	-71	*	*																		
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	206	979	179	350	36	372	585	-636	438	-131	-677	-164	41	73	-335	54	26	12	255	97							
	-3677	-372	2745	60	-4616	-5660	-29	*	*																		
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     1     -70   -217     41   -121  -1232   -394   -611    624   -387  -1326  -1873    158   2390  -1269   -105  -1250    -90    -33  -1451  -1293
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     -   -3259   -161  -9859    -58  -4658  -4637    -59  -5111      *
     2     123   -338    248   1776  -1353    523    869  -1953    251  -1448   -532  -1482    497  -1158  -1652    376   -257  -1133  -1572    228
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     -      -4  -9055 -10055   -732  -1329  -5201    -40      *      *
     3     294   -360    298  -1692   -201    823   -755  -1975   -830    -51  -2016   1103   -187    440   -374   -437  -1313   1364  -1594  -1436
     -     206    979   -179   -352    -36    372    585   -634    438   -130   -675   -164     41    -73   -332    -54     26    -12   -254    -97
     -   -3490   -136 -10090    -53  -4802  -4526    -64      *      *
     4    -510   -433    736  -1764    369   -300   -827   1707   -783   -493  -2088   -690   1083   -581    175  -1466   -126     55  -1667    488
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27	-794	-696	1540	423	-1711	-976	-492	480	-67	397	-870	-143	-219	-111	336	-384	-792	-940	-1930	899
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28	-731	-801	288	-5	-1064	-558	143	1436	-1207	-1104	-640	202	-51	-901	528	-82	1001	-271	-2035	671
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37	369	-803	-897	893	-1167	-244	403	332	-314	577	-2458	-384	693	-740	-471	-1126	207	476	-2037	-1878
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44	210	-763	-892	983	-1778	77	-1157	1046	-1125	-662	-412	790	-771	984	-485	-971	87	601	-1997	-1839
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47	-553	-770	-687	-490	-1464	-1282	1037	796	-900	-382	-1748	233	393	1380	-1037	-730	338	1258	-1456	208
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-	-11	-9685	-7306	-732	-1329	-3640	-121	*	*											
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-	-19	-9727	-6352	-732	-1329	-4033	-91	*	*											
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-	-16	-9720	-6619	-732	-1329	-3672	-118	*	*											
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-	-3	-9735	-10735	-732	-1329	-3920	-99	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9749	-10749	-732	-1329	-4103	-87	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-89	-9562	-4092	-732	-1329	-4716	-56	*	*											
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-	-113	-9474	-3759	-732	-1329	-4259	-77	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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61	233	-449	-245	433	1122	-969	54	-1251	-306	-638	-1112	819	-494	209	-89	-209	820	177	-1338	-302
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-105	-9225	-3861	-732	-1329	-4698	-57	*	*											
62	-542	-412	886	26	304	-988	-806	-196	-483	-446	978	-1275	1877	-515	-1349	270	-653	185	-1646	-841
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-	-81	-9169	-4247	-732	-1329	-4674	-58	*	*											
63	-577	714	-1482	-842	-821	-986	87	297	561	-105	-2035	867	371	-1431	-849	-558	973	1284	-1613	-652
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-	-30	-9118	-5732	-732	-1329	-5214	-39	*	*											
64	-218	-362	591	-710	1123	-969	-537	305	940	-59	-2017	894	-823	-248	532	-818	-630	-89	-456	-1110
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-	-175	-9090	-3155	-732	-1329	-5239	-39	*	*											
65	-379	-251	636	-1582	607	-858	-645	882	-303	-303	-1907	59	65	-1303	-938	-636	-208	1745	-1485	-1327
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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68	-879	-136	740	-234	146	-743	668	128	-154	83	-1791	949	696	-126	-1055	-1115	348	666	-1370	-1212
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-	-216	-8338	-2878	-732	-1329	-5530	-32	*	*										
76	407	179	-935	384	1376	-401	-215	-1380	499	-446	-1477	-965	1226	2	-232	155	-329	-768	-1055	-897
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77	-457	316	-841	-1015	1901	-291	-78	-1298	-225	-793	-1339	-827	2057	-736	-998	-717	472	26	-918	-759
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-	-438	-7805	-1957	-732	-1329	-5702	-28	*	*										
78	-281	492	-665	-171	1368	-115	98	-956	804	-352	-1164	-651	-446	818	81	-541	-149	240	970	-584
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79	-107	666	-492	-665	2478	59	272	-948	125	-443	-990	-477	-272	-386	-648	-367	-286	-325	-568	-410
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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RF    no
CS    no
COM   [converted from an old Plan9 HMM]
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DATE  Mon Mar  8 11:43:15 1999
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NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

        m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
       -5111      *    -42
    1    -70   -217     41   -121  -1232   -394   -611    624   -387  -1326  -1873    158   2390  -1269   -105  -1250    -90    -33  -1451  -1293
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    -  -3259   -161  -9859    -58  -4658  -4637    -59  -5111      *
    2    123   -338    248   1776  -1353    523    869  -1953    251  -1448   -532  -1482    497  -1158  -1652    376   -257  -1133  -1572    228
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    -     -4  -9055 -10055   -732  -1329  -5201    -40      *      *
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    -    206    979   -179   -352    -36    372    585   -634    438   -130   -675   -164     41    -73   -332    -54     26    -12   -254    -97
    -  -3490   -136 -10090    -53  -4802  -4526    -64      *      *
    4   -510   -433    736  -1764    369   -300   -827   1707   -783   -493  -2088   -690   1083   -581    175  -1466   -126     55  -1667.    488
    -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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    -  -3707   -116 -10307    -46  -4980  -5467    -33      *      *
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-	-3	-9515	-10515	-732	-1329	-5160	-41	*	*											
13	-821	-656	360	1728	81	-911	-173	260	-326	-1766	-2312	-1491	-717	333	857	-69	852	-829	-1890	-798
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-51	-9527	-4914	-732	-1329	-4925	-48	*	*											
14	-144	-641	-761	-1973	1696	-335	410	1135	-486	-1413	-785	-1785	302	-1618	228	-395	674	363	-1876	879
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-256	-9507	-2632	-732	-1329	-4097	-87	*	*											
15	380	-541	1053	-992	735	-221	-8	352	-991	-1044	-1868	-306	320	-1398	156	217	1171	-1398	-1775	-8
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-	-10	-9449	-7518	-732	-1329	-4497	-65	*	*											
19	-385	-634	1013	594	312	279	-651	617	-181	14	-2290	56	-720	-289	-333	-1602	492	-223	-146	-785
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9501	-10501	-732	-1329	-5142	-41	*	*											
20	-768	-639	1117	-899	-1654	-115	-1033	812	726	-676	-1546	808	297	-894	644	203	-95	-354	-1873	-1715
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9507	-10507	-732	-1329	-4717	-56	*	*											
21	-225	-654	-487	271	-139	-304	652	335	-189	-1763	-2309	288	419	-830	1052	538	-1044	901	-1888	-878
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-39	-9526	-5289	-732	-1329	-4526	-64	*	*											
22	-537	-657	-157	1082	648	-998	-354	-481	770	-194	-2190	158	437	674	-1388	-775	897	-473	-1891	-1665
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-81	-9531	-4236	-732	-1329	-4117	-86	*	*											
23	-936	-661	5	-1422	409	-608	252	-363	29	-92	-796	403	900	1083	25	-28	559	55	-128	-953
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-104	-9537	-3874	-732	-1329	-3502	-133	*	*											
24	-736	46	379	267	950	296	279	424	572	-331	-2331	-159	-1371	934	561	-829	-986	-57	-1909	-1751
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-3	-9553	-10553	-732	-1329	-3494	-134	*	*										
25	-862	-765	757	-103	407	-276	-615	-630	-57	-482	-647	33	252	339	680	-571	733	-52	-1999	641
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-50	-9677	-4930	-732	-1329	-3921	-99	*	*										
26	-1526	-753	-143	400	1231	-204	1618	1162	-1294	411	-1739	-518	-751	-121	-684	-458	260	-516	566	-1828
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-129	-9660	-3563	-732	-1329	-3973	-95	*	*										
27	-794	-696	1540	423	-1711	-976	-492	480	-67	397	-870	-143	-219	-111	336	-384	-792	-940	-1930	899
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9581	-10581	-732	-1329	-3282	-157	*	*										
28	-731	-801	288	-5	-1064	-558	143	1436	-1207	-1104	-640	202	-51	-901	528	-82	1001	-271	-2035	671
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9725	-10725	-732	-1329	-4450	-68	*	*										
29	-777	-801	182	1268	-173	-178	-1147	302	651	-540	-2456	651	-910	-1853	598	-633	490	78	-2035	-1877
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-69	-9725	-4461	-732	-1329	-4450	-68	*	*										
30	636	-751	-512	97	198	187	-1145	-2365	-97	-414	629	-190	403	-68	-1425	477	984	118	-1985	-1827
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-145	-9657	-3401	-732	-1329	-3642	-120	*	*										
31	578	-700	-1411	514	-1342	638	-1094	1053	-1040	-462	-2355	-315	-1638	-25	-568	336	658	40	-1934	106
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-42	-9587	-5173	-732	-1329	-3125	-176	*	*										
32	-1286	-775	-159	94	-883	339	677	671	-205	342	-1957	-1206	-1714	1310	12	-701	553	-478	-2009	1069
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
33	437	-775	793	-55	-1791	732	-1170	258	-772	324	336	523	-1714	-1541	164	89	-105	-413	-2009	-1041
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
34	-1082	-775	12	-38	-1153	-1155	-345	38	481	362	353	-1097	-127	279	491	210	676	321	-1480	-14
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
35	-96	-775	224	40	-1514	-210	-1170	370	-82	-216	-37	141	-1714	-342	-258	-133	773	586	-1830	1130
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-3813	-107	*	*										
36	208	-803	-718	-1535	-1192	-1260	-439	38	548	-315	-250	534	-205	-838	333	-82	380	707	872	1268
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9728	-10728	-732	-1329	-4248	-78	*	*										
37	369	-803	-897	893	-1167	-244	403	332	-314	577	-2458	-384	693	-740	-471	-1126	207	476	-2037	-1878
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-9728	-6438	-732	-1329	-3886	-101	*	*										
38	391	-806	169	-1716	-103	-229	-1200	-1149	7	588	219	953	631	414	-668	-377	558	-532	-2040	-1158
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-49	-9732	-4964	-732	-1329	-3907	-100	*	*										
39	-307	-783	458	-1517	-1799	-1341	-2	558	-498	705	-425	517	669	504	230	-250	-300	-261	-2017	671

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-46	-9702	-5048	-732	-1329	-3638	-121	*	*											
40	50	-786	1003	109	-1801	-426	54	240	-651	-53	-2442	-1008	236	-1838	1520	304	-1323	429	-2020	-1862
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-13	-9705	-7013	-732	-1329	-3668	-118	*	*											
41	183	-810	-742	1011	-731	334	-404	-928	-942	650	-2466	-642	-1206	-122	903	-1843	-285	583	-181	518
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-78	-9738	-4286	-732	-1329	-4247	-78	*	*											
42	-75	-754	1094	476	-1769	-500	-203	-21	-1295	-1814	-2410	427	-511	228	853	818	591	-36	-1988	-1830
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-194	-9661	-3003	-732	-1329	-3478	-136	*	*											
43	681	-676	620	490	-1319	-627	-137	-1627	-250	-137	-1056	313	-38	-201	1005	-896	516	-721	-1910	505
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-77	-9553	-4305	-732	-1329	-2989	-194	*	*											
44	210	-763	-892	983	-1778	77	-1157	1046	-1125	-662	-412	790	-771	984	-485	-971	87	601	-1997	-1839
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-80	-9675	-4254	-732	-1329	-3369	-147	*	*											
45	-219	-766	-596	135	-652	397	-803	1168	208	-647	-2422	143	-2	-56	2	-371	871	-475	927	-1842
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-61	-9679	-4629	-732	-1329	-3690	-116	*	*											
46	-545	-192	468	-562	-1470	344	995	-2038	-1190	154	942	23	-1466	881	-83	-576	387	968	-489	118
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-42	-9663	-5177	-732	-1329	-3620	-122	*	*											
47	-553	-770	-687	-490	-1464	-1282	1037	796	-900	-382	-1748	233	393	1380	-1037	-730	338	1258	-1456	208
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-9685	-7306	-732	-1329	-3640	-121	*	*											
48	-249	-801	1173	215	-935	-507	402	-244	-1342	366	-2334	706	343	-6	-2065	-750	-192	452	-1819	975
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-19	-9727	-6352	-732	-1329	-4033	-91	*	*											
49	-96	-793	1036	-666	-112	-1381	431	-1079	-250	-1178	357	934	-1198	-594	98	-383	386	1436	-2028	-187
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-20	-9716	-6290	-732	-1329	-3835	-105	*	*											
50	-530	-796	-1474	-158	-632	-397	-306	143	-451	117	-1431	1265	-430	-345	-963	-124	210	1212	-1882	858
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-16	-9720	-6619	-732	-1329	-3672	-118	*	*											
51	-733	-807	872	151	-609	-831	-1202	512	-1085	174	-1417	315	265	-118	588	-1327	680	830	-2042	-1883
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9735	-10735	-732	-1329	-3920	-99	*	*											
52	-289	137	440	-429	-1245	-1425	-1212	1239	-34	265	-569	396	369	-659	-16	-1851	-269	953	-2052	-89
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9749	-10749	-732	-1329	-4103	-87	*	*											
53	-55	947	236	380	-588	-389	-213	41	-361	-540	-323	1115	219	-174	-711	-495	662	403	-2052	-1894
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-92	-9749	-4041	-732	-1329	-4103	-87	*	*											

54	159	-751	289	572	77	-55	-1145	105	-1292	-296	-2407	774	1059	-615	-509	-669	-481	876	-1985	-1827
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-64	-9658	-4566	-732	-1329	-4532	-64	*	*											
55	-100	-705	-318	-214	-883	-598	-538	263	-101	33	-907	1116	922	-114	-334	25	135	404	-1939	-1530
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-35	-9595	-5473	-732	-1329	-4636	-59	*	*											
56	381	44	1665	302	216	-653	-941	-1411	74	-621	-1801	887	-678	-512	-1461	-755	766	80	-1916	-1758
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-89	-9562	-4092	-732	-1329	-4716	-56	*	*											
57	-172	-619	1279	-377	186	-1077	-1014	3	-313	-1034	-1877	1066	480	-330	-381	-345	649	640	-1854	-1695
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-113	-9474	-3759	-732	-1329	-4259	-77	*	*											
58	124	-583	405	-1093	-1552	109	-977	109	563	-1050	-2238	2002	686	-1084	-756	-523	-53	121	-1817	-897
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-45	-9421	-5099	-732	-1329	-4991	-46	*	*											
59	12	-553	1111	-1011	-1	-252	-764	-1203	189	-1388	-916	989	1288	-411	-829	-619	692	-192	-1787	458
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-54	-9379	-4829	-732	-1329	-4725	-56	*	*											
60	-391	-531	230	-158	63	80	360	691	-984	-484	-2187	1022	1232	-1090	-1776	-602	518	426	-1765	-1607
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-122	-9346	-3652	-732	-1329	-5120	-42	*	*											
61	233	-449	-245	433	1122	-969	54	-1251	-306	-638	-1112	819	-494	209	-89	-209	820	177	-1338	-302
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-105	-9225	-3861	-732	-1329	-4698	-57	*	*											
62	-542	-412	886	26	304	-988	-806	-196	-483	-446	978	-1275	1877	-515	-1349	270	-653	185	-1646	-841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-81	-9169	-4247	-732	-1329	-4674	-58	*	*											
63	-577	714	-1482	-842	-821	-986	87	297	561	-105	-2035	867	371	-1431	-849	-558	973	1284	-1613	-652
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-30	-9118	-5732	-732	-1329	-5214	-39	*	*											
64	-218	-362	591	-710	1123	-969	-537	305	940	-59	-2017	894	-823	-248	532	-818	-630	-89	-456	-1110
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-175	-9090	-3155	-732	-1329	-5239	-39	*	*											
65	-379	-251	636	-1582	607	-858	-645	882	-303	-303	-1907	59	65	-1303	-938	-636	-208	1745	-1485	-1327
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-113	-8912	-3777	-732	-1329	-5382	-35	*	*											
66	-886	-183	-1213	-221	-647	-790	-161	-915	239	352	-1839	1571	-1122	594	683	-954	492	727	-1417	-444
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8801	-9801	-732	-1329	-5421	-34	*	*											
67	-353	-27	1175	-1514	276	-790	-577	958	125	110	-1839	-1327	632	-1235	-1497	-567	-137	1162	-1417	-1259
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-82	-8801	-4232	-732	-1329	-5421	-34	*	*											
68	-879	-136	740	-234	146	-743	668	128	-154	83	-1791	949	696	-126	-1055	-1115	348	666	-1370	-1212
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-5	-8719	-9719	-732	-1329	-5443	-34	*	*										
69	-506	-136	1261	-117	-76	-440	-530	9	177	-616	-1313	614	336	-58	-1450	-1169	-1088	1457	-1370	-1212
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-109	-8719	-3824	-732	-1329	-5443	-34	*	*										
70	38	-73	1252	-672	468	-406	133	-263	-592	-671	-1149	974	677	-979	-1388	-279	72	670	-1308	-1149
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-103	-8610	-3914	-732	-1329	-5476	-33	*	*										
71	-790	-17	2062	-696	-1032	-624	-411	-867	-558	-1126	-1673	2130	-956	-1069	292	-1050	-970	388	-1251	-1093
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8506	-9506	-732	-1329	-5497	-32	*	*										
72	175	-17	1314	-452	913	-624	-411	-179	-325	-1066	-1673	1683	218	137	-1331	-677	-204	-418	-1251	-1093
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-162	-8506	-3271	-732	-1329	-5497	-32	*	*										
73	-379	71	849	-780	-675	-536	-5	-1544	-471	-553	-1585	2472	1258	-981	-1058	-241	-882	-921	-1163	-1005
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8338	-9338	-732	-1329	-5530	-32	*	*										
74	-33	71	1534	73	-944	-536	806	-1282	188	-1039	-1585	732	1809	-981	-244	-962	-882	-921	-1163	-1005
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8338	-9338	-732	-1329	-5530	-32	*	*										
75	-331	71	-1087	-654	975	275	464	-801	-471	-1039	-1585	1561	1660	-328	58	-713	-132	-680	-1163	-1005
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-216	-8338	-2878	-732	-1329	-5530	-32	*	*										
76	407	179	-935	384	1376	-401	-215	-1380	499	-446	-1477	-965	1226	2	-232	155	-329	-768	-1055	-897
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-304	-8119	-2422	-732	-1329	-5608	-30	*	*										
77	-457	316	-841	-1015	1901	-291	-78	-1298	-225	-793	-1339	-827	2057	-736	-998	-717	472	26	-918	-759
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-438	-7805	-1957	-732	-1329	-5702	-28	*	*										
78	-281	492	-665	-171	1368	-115	98	-956	804	-352	-1164	-651	-446	818	81	-541	-149	240	970	-584
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-522	-7424	-1749	-732	-1329	-5819	-26	*	*										
79	-107	666	-492	-665	2478	59	272	-948	125	-443	-990	-477	-272	-386	-648	-367	-286	-325	-568	-410
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
-	*	*	*	*	*	*	*	*	0										

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RF    no
CS    no
COM   [converted from an old Plan9 HMM]
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NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
         -2108      *   -381
      1   -750     23   1183   1324   -992   -584   2548  -1592    398   -334  -1633  -1121   -916   1235  -1291  -1010   -930   -969  -1211  -1053
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8487  -9487   -732  -1329  -3382   -146  -2108      *
      2   -750     23  -1135  -1308   -992   -584   -371  -1592    971   1557  -1633  -1121   -916   2302  -1291  -1010   -930   -969  -1211  -1053
      -    206    979   -179   -351    -36    372    585   -636    438   -130   -677   -164     40    -73   -335    -54     28    -12   -255    -97
      -  -2887   -212  -9487    -81  -4197  -1685   -538      *      *
      3   -993   -220    -76   1048  -1235   -827   -614  -1834   1812    343  -1875    397  -1158   1001    676  -1253  -1172  -1211  -1454  -1295
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -5  -8911  -9911   -732  -1329  -2684   -244      *      *
      4    910   -247   -394    993  -1262   -854   -641  -1861   1267    515  -1902  -1390  -1185   1683  -1561  -1280  -1199   -327  -1481  -1323
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -4  -8954  -9954   -732  -1329  -1412   -680      *      *
      5  -1190   -417   -178   1870  -1432  -1024   -811  -2031   -958   1137  -2073   -423  -1355   1086    -55  -1450  -1369    711  -1651  -1493
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -4  -9214 -10214   -732  -1329  -1228   -803      *      *
      6   -587   1916  -1694   -882  -1552  -1144   -931    364   1033  -1646    275  -1680  -1475   1923   -650   -585   1131    869  -1770  -1612
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      -     -3  -9387 -10387   -732  -1329   -519  -1728      *      *
      7     95   -682  -1840   1868  -1697  -1289   1372  -2297   1672    290    214  -1826  -1621   -343   -257  -1029  -1635   -338  -1916  -1758
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      -     -3  -9591 -10591   -732  -1329    -33  -5451      *      *
      8   1295   -765  -1923   -159  -1780  -1372  -1159  -2379   1375    363    522  -1908  -1704   1301    909     35  -1717   -715  -1999  -1841
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -3  -9703 -10703   -732  -1329    -76  -4293      *      *
      9    111   -765  -1923    792   -353  -1372  -1159  -1265   1243    613   1797   -437  -1704  -1817   -792   1110  -1717   -324  -1999  -1841
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10	-97	-765	-1923	1931	-1780	-1372	-1159	-2379	889	-205	-2421	834	-1704	462	-2079	42	1031	-633	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
11	678	-765	-1923	1499	19	-1372	-1159	-1003	639	-1874	2448	155	-1704	-338	-1047	255	-862	-1756	-1999	926
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-134	-9703	-3516	-732	-1329	-76	-4293	*	*											
12	-210	-668	-1826	1622	-1683	-1275	-1062	-2283	985	966	-123	551	-1607	-1720	-1982	656	-1621	218	-1902	-1744
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9571	-10571	-732	-1329	-1349	-719	*	*											
13	206	-668	-1826	1035	-1683	-656	-1062	-2283	1500	-1777	-2324	1789	-1607	352	0	769	-299	-1659	-1902	-1744
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-67	-9571	-4507	-732	-1329	-1349	-719	*	*											
14	-400	-622	-1779	214	-1637	-1229	-1016	-2236	1435	18	-2277	1511	-1560	707	-1936	1176	-1574	566	-1856	-1698
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9507	-10507	-732	-1329	-371	-2140	*	*											
15	-1495	-722	191	1199	-1737	-1329	-1116	0	992	53	-2377	622	-1660	1106	-253	-268	276	167	-1956	-1798
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9645	-10645	-732	-1329	-805	-1226	*	*											
16	-334	-722	-1879	-2053	-1737	-1329	-1116	-1221	1902	722	-1115	1658	-1660	-460	355	219	-85	-931	-1956	-1798
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9645	-10645	-732	-1329	-45	-5022	*	*											
17	-95	-765	273	1474	-1780	-1372	-1159	-2379	-1306	-1874	-2421	93	-1704	2190	1291	296	346	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
18	-1538	1686	1504	-1195	-1780	-1372	-1159	-1003	178	1021	522	656	-1704	735	-2079	1006	-862	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
19	-702	-765	391	1171	-1780	-1372	-1159	-2379	353	1472	75	-437	-1704	1354	-2079	468	-1717	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
20	-1538	-765	1375	54	-1780	475	-1159	-2379	510	613	-2421	760	-1704	1066	343	580	-1525	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
21	501	-765	-699	623	-1780	-1372	-1159	-2379	211	1217	-2421	155	-1704	1550	-185	800	-1717	-1756	-1999	-1841
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-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
22	-305	-765	1108	1232	-1780	-1372	1076	476	-1306	-273	-2421	-126	-1704	986	842	509	-843	-1756	-1999	-1841
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-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
23	555	-765	-1923	1559	-1780	-1372	-1159	-40	-1306	884	-2421	1213	-1704	478	-460	-283	271	-1756	-1999	-1841
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-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
24	-1538	-765	1324	2246	-1780	56	269	-2379	-1306	-1874	-2421	324	-1704	547	-308	655	-564	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
25	-960	-765	1587	1219	471	-366	-1159	-2379	685	835	-2421	578	-1704	-563	-196	-1798	-1717	-633	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
26	1010	1823	391	1426	-1780	-1372	1550	-2379	335	633	-2421	-1908	-1704	653	-2079	-823	-739	-1756	-1999	-1841
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-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
27	-346	2080	607	1237	-1780	-1372	-1159	-2379	1321	-205	1633	456	-1704	367	-1043	-431	-601	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
28	780	1949	-1923	1024	-1780	-767	1701	-2379	353	-519	-2421	1209	-1704	-1817	409	-390	717	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
29	-350	-765	-1923	897	-1780	-1372	1011	-2379	820	448	1056	578	-1704	1063	-278	600	344	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
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32	-814	-765	-1923	455	-1780	-1372	1047	142	1853	-306	-2421	975	-1704	993	-348	-1798	795	-485	-1999	-1841
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33	892	-765	-1923	154	-1780	-1372	-1159	805	1126	798	130	927	-1704	597	-2079	-197	-1717	-1022	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-103	-9703	-3885	-732	-1329	-76	-4293	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-78	-9602	-4286	-732	-1329	-1155	-860	*	*										
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-	-131	-9527	-3553	-732	-1329	-1592	-581	*	*										
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-	-3	-9398	-10398	-732	-1329	-992	-1008	*	*										
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-	-3	-9515	-10515	-732	-1329	-800	-1232	*	*										
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-	-115	-9591	-3730	-732	-1329	-33	-5451	*	*										
39	189	920	-304	477	-1704	-1296	1367	-2303	1162	864	1135	167	-1627	254	22	-640	-1017	-1046	-1922	-1764

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-153	-9599	-3328	-732	-1329	-1150	-864	*	*											
40	-612	-575	-1733	724	-1590	-288	-969	229	1435	1452	241	-1718	-1514	-1627	-995	419	-1527	-1311	-1809	-1651
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-	-3	-9433	-10433	-732	-1329	-1874	-459	*	*											
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-	-3	-9433	-10433	-732	-1329	-1874	-459	*	*											
42	806	-575	733	608	-1590	-329	-969	-2189	-115	925	-474	509	-1514	821	-875	-181	-1527	-315	-1809	-1651
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9433	-10433	-732	-1329	-1874	-459	*	*											
43	-114	789	-451	876	-1590	-1182	62	-2189	-1116	1080	-2231	-434	-1514	2299	-218	-167	-1527	-529	-1809	-1651
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-113	-9433	-3756	-732	-1329	-1874	-459	*	*											
44	952	-496	542	-1828	-1512	-401	-891	688	1013	814	1187	-253	-1435	-1548	-542	-779	-1449	-237	-1730	-1572
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-146	-9313	-3401	-732	-1329	-2208	-352	*	*											
45	-1169	-396	943	1796	-1411	-1003	1078	-2010	-57	169	-2051	-343	-1334	94	-1710	845	-1348	126	-1630	-1472
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9112	-10112	-732	-1329	-2511	-278	*	*											
46	-359	-396	1574	341	-1411	92	-790	-694	-937	560	1027	226	-1334	599	129	-1429	468	-1387	-1630	-1472
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-80	-9112	-4263	-732	-1329	-2511	-278	*	*											
47	-186	-345	-714	2004	74	-952	-739	-1182	70	961	48	-1489	-1284	-1397	-1659	347	-1298	-404	-1579	-1421
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9038	-10038	-732	-1329	-2664	-248	*	*											
48	25	908	1639	884	-1360	-412	472	-1575	-886	297	-2001	-1489	-1284	1639	180	-664	-880	-1336	-1579	-1421
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9038	-10038	-732	-1329	-2664	-248	*	*											
49	-498	-345	312	1369	178	994	-739	-1016	-886	33	542	1201	-1284	-1397	168	-398	-1298	-1336	-1579	-1421
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-84	-9038	-4186	-732	-1329	-1978	-422	*	*											
50	271	-346	885	785	-151	-234	-740	-1960	-887	113	-2001	478	179	1231	336	-718	113	-1337	-1580	-1421
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-17	-9041	-6708	-732	-1329	-2719	-238	*	*											
51	-433	-338	-1495	1380	-1353	-945	-732	371	-879	836	255	1009	-1276	-1390	528	265	-1290	-297	-1572	-1413
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9031	-10031	-732	-1329	-2769	-229	*	*											
52	322	-338	-590	1312	-1353	-945	-732	-1952	-879	225	-1993	-1481	-1276	1292	1048	1164	-1102	-1329	-1572	-1413
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9031	-10031	-732	-1329	-2001	-415	*	*											
53	-1161	-388	631	1806	-1403	-146	-782	-2003	-929	413	748	-1532	154	840	252	-580	-1341	-131	-1622	-1464
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-286	-9102	-2488	-732	-1329	-2364	-312	*	*											

54	352	-215	-223	1947	-1230	-822	-609	-1830	-756	-1324	313	-1358	113	1015	952	278	-1168	-1206	-1449	-1291
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-301	-8845	-2427	-732	-1329	-2908	-206	*	*											
55	323	-40	1037	1549	-1056	399	-435	-98	142	-1150	-1696	505	-979	341	-1354	-1005	-146	-1032	-1274	-1116
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-548	-8561	-1674	-732	-1329	-3326	-152	*	*											
56	645	250	436	877	-765	164	-144	-1364	-291	183	-1406	-893	-689	470	-110	-594	-703	630	-984	-826
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-9	-7974	-8974	-732	-1329	-3655	-119	*	*											
57	1091	250	-908	418	-765	445	-144	-62	434	24	-1406	-893	-689	96	-1064	158	133	-741	-984	-826
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-63	-7974	-4692	-732	-1329	-3655	-119	*	*											
58	-497	276	228	-315	-739	379	-118	-1339	582	49	-1380	1411	-663	1081	163	-757	58	-715	-958	-800
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-198	-7928	-3011	-732	-1329	-3691	-116	*	*											
59	705	361	-797	326	-654	-246	-33	-920	-181	755	-1295	-783	-578	-691	-953	934	332	-631	-873	-715
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-160	-7709	-3319	-732	-1329	-3759	-111	*	*											
60	187	425	-452	204	-590	424	31	-1189	385	28	-1230	-718	-513	-627	1072	205	448	-566	-809	-650
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-330	-7581	-2328	-732	-1329	-3828	-105	*	*											
61	-226	548	-610	286	-468	-60	153	-1067	6	-406	-1108	-596	-391	1784	-767	1078	-405	-444	-687	-528
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-449	-7247	-1937	-732	-1329	-3913	-99	*	*											
62	653	696	-462	412	-319	89	302	146	155	-239	-960	-447	-242	-356	616	-337	-256	-295	-538	-380
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-19	-6860	-7860	-732	-1329	-4022	-92	*	*											
63	-77	696	-462	390	-319	89	302	-918	155	308	-960	-447	-242	966	-618	-337	671	-295	-538	-380
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
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DATE  Mon Mar  8 11:40:16 1999
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NULT      -4  -8455
NULE     595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM        A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

         m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
         -202      *  -2939
     1    179    953   -205     84    -63    345    558   -662    411   -157   -703   -191     14   -100   -362    -81      0    -39   -282   -123
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -39  -5797  -6797   -732  -1329  -1611   -572   -202      *
     2    179    953   -205   -379    -63    345    558   -662    411   -157   -703   -191     14   -100   -362    -81    400    -39   -282   -123
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -39  -5797  -6797   -732  -1329  -1369   -707      *      *
     3    150    923   -234    110    -92    316    529   -691    382   -186   -732    313    -15   -129   -391   -110    -29    -68   -311   -152
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -36  -5924  -6924   -732  -1329  -1478   -642      *      *
     4    150    923   -234   -408    -92    316    529   -691    382   -186   -732   -220    -15   -129    137   -110    420    -68   -311   -152
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -36  -5924  -6924   -732  -1329  -1478   -642      *      *
     5    150    923   -234   -408    -92    316    529   -691    382   -186   -732    393    -15   -129   -391   -110    -29    287   -311   -152
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -36  -5924  -6924   -732  -1329  -1478   -642      *      *
     6    150    923   -234   -408    -92    584    529   -691    382   -186   -732   -220    -15   -129    217   -110    -29    -68   -311   -152
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -36  -5924  -6924   -732  -1329  -1478   -642      *      *
     7    150    923   -234   -408    -92    316    529   -691    382   -186    181   -220    -15   -129   -391    223    -29    107   -311   -152
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -36  -5924  -6924   -732  -1329  -1478   -642      *      *
     8    150    923   -234   -408    -92    628    529   -691    382   -186   -732    313    -15   -129   -391   -110    -29    -68   -311   -152
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -36  -5924  -6924   -732  -1329  -1478   -642      *      *
     9    150    923   -234   -408    -92    316   1150   -691    382   -186   -732   -220    -15   -129   -391    277    -29    -68   -311   -152
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -36  -5924  -6924   -732  -1329  -1478   -642      *      *
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10	150	923	-234	-408	-92	584	529	-691	382	-186	-732	51	-15	-129	-391	138	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
11	150	923	-234	-408	-92	316	1240	-116	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
12	351	923	-234	-408	-92	446	529	-691	382	-186	-732	313	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
13	150	923	-234	-408	-92	316	529	-213	382	-186	-732	-220	-15	429	-391	-110	-29	78	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
14	150	923	-234	-408	-92	316	529	-691	382	-186	-732	763	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
15	150	923	-234	-408	-92	316	529	-691	382	-186	-732	-220	-15	512	-391	-110	-29	287	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
16	150	923	-234	-408	-92	316	529	-691	382	-186	-732	393	-15	-129	-391	223	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
17	150	923	-234	-408	-92	316	529	-691	382	-186	-732	-220	-15	429	-391	-110	-29	344	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
18	150	923	-234	-408	-92	316	529	-691	382	-186	-732	183	-15	-129	-391	355	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
19	150	923	-234	-408	-92	316	529	-691	382	91	-732	-220	-15	512	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
20	150	1546	-234	-408	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	277	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
21	150	923	-234	-408	-92	316	529	-691	382	137	-732	-220	-15	429	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
22	150	1637	-234	41	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
23	150	923	236	-408	-92	316	529	-691	382	-186	-732	-220	-15	512	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
24	150	923	236	110	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
25	150	923	308	-408	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	529
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
26	150	923	308	41	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-165	-5924	-3451	-732	-1329	-1478	-642	*	*											
27	175	948	-210	-383	-67	341	554	-667	406	-162	-708	-196	9	-104	-366	-85	-5	-44	-286	668
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-39	-5810	-6810	-732	-1329	-1589	-583	*	*											
28	175	948	-210	147	-67	341	554	-667	406	-162	-708	-196	9	-104	-366	-85	-5	-44	-286	-128
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NY02:195620.1

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CS    no
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
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          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
          -552      *  -1653
      1   2062     13  -1144  -1318    244   -594   -381  -1601   1755  -1096  -1642  -1130   -925  -1039  -1301  -1020   -939   -177  -1221   -628
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8523  -9523   -732  -1329   -543  -1673   -552      *
      2   -780     -7   2178  -1338  -1022    180   -401  -1621   -548  -1116    954  -1150   -946   2132    467  -1040   -960   -998  -1241  -1083
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8558  -9558   -732  -1329   -630  -1499      *      *
      3   -780     -7  -1165  -1338  -1022   1560   -401  -1621   -275  -1116    954  -1150   -946  -1059   -197   1800   -960    353  -1241  -1083
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8558  -9558   -732  -1329   -630  -1499      *      *
      4   1737     -7  -1165  -1338  -1022   -614   -401  -1621   -548  -1116    954   2386   -946  -1059   -762  -1040   -128   -998  -1241  -1083
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8558  -9558   -732  -1329   -630  -1499      *      *
      5   -193   3780  -1165    259  -1022    277   -401  -1621   -548  -1116  -1663  -1150   -441  -1059  -1321   1412   -960   -998  -1241  -1083
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8558  -9558   -732  -1329   -412  -2010      *      *
      6   -797    -23  -1181   1916  -1039   -631   -418   -888   -565    269  -1679  -1167   1874   -401  -1338      5   -976  -1015  -1257  -1099
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8587  -9587   -732  -1329    -57  -4687      *      *
      7     73    -56   2129  -1388  -1071   -663   -451  -1671   -598    -44  -1712   1921   -995    323  -1370  -1090  -1009     -1  -1290  -1132
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -5  -8644  -9644   -732  -1329    -76  -4293      *      *
      8   -830    -56  -1214  -1388  -1071   -663   -451   -500   -598    -44   -363  -1200   2247   -324   -249  -1090  -1009   1721  -1290  -1132
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -   -646  -8644  -1480   -732  -1329    -76  -4293      *      *
      9   -491    283   -875  -1049   -733   -325   -112  -1332   -259    295   1953   -861   -656   2423  -1032   -751   -670    408   -951   -793
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -8  -8004  -9004   -732  -1329  -2034   -404      *      *
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10	411	283	2060	-1049	-733	-325	1883	-1332	103	-827	1710	-861	-656	-770	-1032	-751	-670	-709	-951	-793
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-763	-8004	-1298	-732	-1329	-2034	-404	*	*											
11	-182	591	-566	597	74	1526	197	-1023	50	-176	344	-552	-347	-461	-723	-442	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
12	924	591	-566	-740	-424	765	197	-1023	50	397	-1065	-552	-347	-461	-723	551	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
13	659	591	-566	858	-424	-16	197	-1023	50	397	-1065	219	-347	-461	-723	147	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
14	98	591	-566	-740	-424	-16	197	-1023	50	397	-1065	-552	1474	681	-85	-442	-108	-278	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
15	67	591	-566	-193	-424	-16	424	-1023	50	397	-1065	1248	-347	-294	-298	-442	-361	646	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
16	659	2591	-566	-740	-424	-16	1897	-79	50	-518	-1065	-552	-347	-461	-723	-442	-361	143	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
17	1345	591	-566	518	-424	874	197	-1023	50	-518	-1065	-552	-347	-461	-723	-442	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
18	769	591	1085	-278	-424	-16	197	-1023	50	481	-1065	-552	-347	-461	-83	-442	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
19	-182	591	-566	775	-424	-16	197	-1023	50	548	-1065	-552	1229	-461	-83	-442	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-376	-7251	-2166	-732	-1329	-2653	-250	*	*											
20	-67	707	-451	-625	-309	99	312	-908	165	948	-949	-437	1085	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
21	-67	707	-451	-625	-309	99	312	-908	165	948	-949	1084	-232	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
22	-67	2411	-451	-625	-309	99	1921	-908	432	168	-949	-246	-232	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
23	835	707	-451	-625	-309	929	948	-908	165	-403	-949	-437	-232	168	32	-327	-246	-285	-527	-117
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
24	774	707	935	-625	-309	879	312	-908	165	-403	-949	-437	-232	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
25	723	707	-451	633	-309	99	312	-908	165	-403	-949	-437	1085	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-367	-6891	-2210	-732	-1329	-2810	-222	*	*											
26	27	800	-192	-71	-215	193	406	-815	259	-310	-856	302	1100	-252	-514	71	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*											
27	27	800	-358	-531	-215	193	406	-815	259	-310	-856	1092	959	-252	-514	-119	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*											
28	27	2413	26	-531	-215	193	406	-815	259	-310	-856	805	-139	-252	-514	-233	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*											
29	867	1588	-358	-531	-215	193	406	-815	259	32	-856	-344	-139	-252	-514	-233	-153	133	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*											
30	306	800	947	-374	-215	193	406	-815	619	-310	-856	-344	-139	261	-514	-233	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*											
31	27	800	878	-531	-215	193	406	-815	259	-310	-856	-344	1100	-252	-514	-233	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-731	-6546	-1370	-732	-1329	-2921	-204	*	*											
32	171	944	-213	-387	-71	337	550	-670	403	-165	-712	-199	576	-108	-370	-89	-8	-47	-290	-132
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
-	*	*	*	*	*	*	*	*	0											

//

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HMMER2.0
NAME Dhr1.txt
DESC
LENG  54
ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:43:47 1999
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
         -1144      *   -869
     1    -501      7   -618  -1985    -97    281   -409   1925   -295    189  -1742  -1334  -1202    -56  -2169   -671   -701   1400  -1760  -1089
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -43 -12932  -5112   -732  -1329   -983  -1017  -1144      *
     2    -634   -614   -105   -796    760    727  -1553   1245    -25   -818  -2691   -843   -601  -1338   -123    -48   -593    855  -4869   1049
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -       0 -12944 -13944   -732  -1329   -357  -2191      *      *
     3    -341    820   -169  -2147  -1458    263  -1110   1629   -851   -362  -1805  -1355    -53   -507   -528   -622   -478   1758  -4942  -1259
     -     205    976   -178   -354    -39    374    583   -628    438   -133   -677   -163     37    -75   -333    -53     28     -8   -261    -94
     -   -7420    -13   -8263     -3  -8720  -1883   -456      *      *
     4    -150  -2770    410   -134   -623    715   -228    680     46   -580  -1079   -269   -679    111   -501    729  -2038    895  -4928  -1317
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -16 -13006  -6495   -732  -1329  -1039   -962      *      *
     5     260  -2763   -285   -935  -1072    383   -380   1383   -649   -111    693   -333    412    219   -682   -766  -2749   1203  -1858  -2122
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -16 -13004  -6516   -732  -1329  -1434   -667      *      *
     6     559  -2762    822   -321  -1370   1043   -259     16   -176    188    938   -502   -671    163   -411   -484   -783     43  -4920  -2754
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -33 -12997  -5463   -732  -1329   -615  -1527      *      *
     7     349  -1925    666     78  -3109    743    999   -381    120  -1005  -5338   -358   1253     98   -484   -219   -734    583  -4916  -4758
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -11 -12993  -7000   -732  -1329   -733  -1328      *      *
     8     350  -1175    306     -4  -1162   1723   -417    525   -745   -510  -3747    508     70    219   -566   -360  -1044   -883  -4932  -3211
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -18 -13009  -6311   -732  -1329  -1499   -630      *      *
     9     882    157    396   -424  -2651   1520   -542   -508   -802   -901  -1066  -1683    356   -110   -954    775   -773     -7  -1821  -2893
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -14 -12998  -6677   -732  -1329   -918  -1087      *      *
```

10	1318	-1935	340	148	-1357	581	-1091	-86	-690	-381	-254	-57	1369	-368	-566	-247	-3102	-422	-1823	-3765
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-54	-13004	-4771	-732	-1329	-728	-1335	*	*											
11	1893	-639	-218	44	-1473	718	148	-311	-659	-351	-1770	-215	-1734	38	-854	-105	-1670	56	-1791	-4737
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-25	-12971	-5888	-732	-1329	-759	-1289	*	*											
12	978	-693	905	700	-2164	332	142	-44	-758	-383	-2272	-128	76	557	-1	-478	-2207	107	-1807	-1809
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-22	-12986	-6078	-732	-1329	-777	-1264	*	*											
13	805	-168	209	-366	-4699	557	-50	-935	937	26	-498	515	-2117	370	764	-839	-799	20	-4918	-2103
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-60	-12995	-4619	-732	-1329	-775	-1267	*	*											
14	584	275	1084	-322	-1250	1064	-664	-240	-295	-85	-466	-1322	-2121	402	5	358	-1242	19	-1786	-2505
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-60	-12961	-4611	-732	-1329	-473	-1839	*	*											
15	-1034	-624	386	-20	-2342	1988	33	367	-109	-199	162	-171	-1634	-588	307	-384	-1724	-119	-4884	-4726
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-128	-12960	-3565	-732	-1329	-510	-1747	*	*											
16	139	-963	1082	-542	-1824	244	-581	-344	134	129	-475	186	-984	354	1129	-268	-227	-31	-4815	-4657
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-22	-12888	-6063	-732	-1329	-541	-1677	*	*											
17	-350	-1679	-154	-190	-914	678	306	1357	-976	1179	118	-1391	-3267	140	-24	-1324	-587	164	-4922	-4764
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-21	-12999	-6119	-732	-1329	-831	-1191	*	*											
18	-506	83	276	282	-2197	318	1173	365	465	-288	-2944	-87	-1223	932	1004	-387	-1297	332	-4922	-3758
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-12998	-8242	-732	-1329	-440	-1927	*	*											
19	-27	-1188	830	-116	-946	277	152	639	136	-6	-124	347	288	-269	-161	-820	-1276	540	-931	-2932
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-13024	-7032	-732	-1329	-1606	-575	*	*											
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 -   *     *     *     *     *     *     *      *      *     *      *      *     *      *     *     *      *     *      *     *
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ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:44:03 1999
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y
          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
        -3130      *   -175                 *
      1   -235    539   -619   -793    463    -69    144    371     -3    301    634   -605   -400    545   -776   -495   1111   -453   -695    537
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12    255     97
      -    -13  -7388  -8388   -732  -1329  -3508   -133  -3130      *
      2    308    539   -619      4    539    -69    144   -205     -3    627  -1117    178    445   -513   -776   -495   -414     93   -695   -537
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      -    -13  -7388  -8388   -732  -1329  -3010   -191      *      *
      3   -289    485   -673     17   -530   -122     91   -710    523    -54    420    717   -454   -567   -829    740    456      7   -749   -591
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      -    -12  -7519  -8519   -732  -1329  -3171   -170      *      *
      4     99   1519   -701   -875    559    328     62    -71    -85   -653  -1199    776    888   -595   -858    360    257   -535   1482    619
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      -    -11   7588  -8588   -732  -1329  -3409   -143      *      *
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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17	83	457	-701	-875	99	-151	62	652	454	-159	454	293	-482	-595	-858	498	-38	318	-777	619
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-	-11	-7588	-8588	-732	-1329	-3409	-143	*	*											
18	-317	457	6	-875	207	346	62	138	930	-653	126	506	-482	-595	32	622	-318	535	777	619
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-	-11	-7588	-8588	-732	-1329	-3409	-143	*	*											
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-	-11	-7588	-8588	732	1329	3409	-143	*	*											
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-	-11	7588	8588	732	1329	3409	-143	*	*											
21	317	457	-701	325	559	690	62	-1158	515	-653	-1199	-687	359	432	-858	598	-19	528	-777	-619
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22	21	457	-31	542	-559	404	62	-1158	514	-225	-1199	94	149	432	32	-577	202	-97	-777	-619
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7588	-8588	-732	-1329	-3409	-143	*	*											
23	-317	457	101	-875	985	402	62	-71	583	-653	-1199	630	172	-595	-232	-297	626	-535	-777	-619
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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24	-317	1519	358	-875	456	404	62	-73	360	206	-1199	-35	1070	-595	-858	-450	-496	-535	-777	-619
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25	104	1603	-701	655	-559	402	62	-307	53	-653	-1199	-687	-482	1022	-858	526	178	-535	-777	-619
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-	-11	-7588	-8588	-732	-1329	-3409	-143	*	*											
26	83	457	-126	1	-559	-151	1121	-1158	-85	-653	-1199	-687	543	976	-858	1004	277	-535	-777	-619
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7588	-8588	-732	-1329	-3409	-143	*	*											
27	169	1586	-701	-875	472	244	1205	-320	499	-653	-1199	-687	-279	-595	-858	404	275	-535	-777	1063
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-	-11	-7588	-8588	-732	-1329	-3140	-174	*	*											
28	-344	1592	299	256	892	-178	35	174	-112	176	-1227	-714	-243	-623	-885	-119	174	-562	-805	590
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7653	-8653	-732	-1329	-3378	-146	*	*											

29	141	1590	-729	-259	-586	-178	35	-1185	875	-337	-1227	171	-510	1473	94	-604	481	-562	805	647
-	206	979	-178	-352	-36	372	585	-635	438	130	-677	-164	41	-73	-335	-54	27	12	255	97
-	-11	-7653	-8653	-732	-1329	-2849	-215	*	*											
30	-404	369	585	-962	-646	-238	1134	-1245	190	675	-1287	19	-569	1384	-171	-57	-583	-106	865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
31	-404	1285	524	46	116	-238	1132	-308	1	13	-1287	-774	-569	-683	326	-1	114	-87	-865	548
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
32	124	369	41	-318	-646	-238	-25	-1245	272	557	-404	-535	-569	-613	-362	-429	1259	-184	865	546
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-70	-7794	-4535	-732	-1329	-3313	-153	*	*											
33	-378	396	552	-386	-619	-211	1	-370	769	-714	-1260	1065	-543	403	-918	19	214	322	838	143
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
34	165	2276	-762	-167	198	-211	1	-381	443	-380	-1260	46	-543	401	-918	960	-557	596	838	-680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
35	397	1532	-762	-738	-619	504	1060	-1219	-146	-370	489	-310	122	-656	-292	566	216	95	-838	-680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
36	-378	396	693	-936	-619	121	1144	-228	307	-714	-1260	885	-543	-656	-918	-146	971	596	-838	969
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7735	8735	732	1329	-3346	-149	*	*											
37	397	1758	649	960	-619	-211	752	311	39	-714	270	-748	-543	-656	68	-638	-557	-596	-838	680
-	206	979	178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
	10	7735	8735	732	1329	3346	-149	*	*											
38	397	396	683	936	784	-211	1	141	453	-714	-741	-748	-543	-656	61	818	-78	-576	-838	-680
-	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	97
-	-10	7735	-8735	-732	-1329	-3346	-149	*	*											
39	126	396	-89	234	758	-211	1161	-368	299	-158	-1260	-748	-543	-656	-134	164	-557	261	-838	434
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
42	169	396	151	-924	852	-211	1028	-1219	997	-714	472	255	-543	-656	469	-638	81	107	-838	-680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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44	956	369	-788	-207	-646	-238	-25	-1245	1219	-179	-1287	-421	-569	251	-945	-640	528	92	-865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7794	-8794	732	1329	-3313	-153	*	*											
45	627	369	-81	223	646	-238	25	844	417	69	1287	244	185	-683	945	-664	-583	91	-865	707
	206	979	178	352	36	372	585	635	438	-130	-677	-164	41	-73	335	-54	27	12	-255	97

-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
46	550	369	13	-962	353	-238	-25	-262	-172	389	-1202	242	-569	-340	638	254	-405	87	885	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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47	148	369	-100	442	-646	495	-25	-1245	771	117	-1287	-730	266	-683	63	-179	-583	359	865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	-97
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48	-404	369	-788	-99	-646	94	-25	310	724	404	-1287	122	-569	132	130	-7	164	-622	-865	287
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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49	-404	369	-788	-690	-646	171	-25	1063	833	386	-1287	-774	-569	-5	-945	263	-583	-387	865	911
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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50	197	1310	-76	-136	198	134	15	-1206	374	-139	-1247	347	-530	-643	-894	28	-544	113	-825	1433
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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51	-404	1823	-652	1115	-646	-124	272	-1245	280	-170	-1287	-447	-569	-683	385	-12	-583	-87	-865	1131
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
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52	963	369	-788	633	-391	-238	-25	385	366	-570	850	-774	-569	-683	-945	-664	-583	390	-865	530
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53	404	369	-788	486	-601	187	-25	1072	733	404	-1287	-774	-569	-683	-945	-12	-22	-622	-865	60
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54	404	369	788	547	816	171	416	629	-172	509	-1287	-18	-569	314	-945	-664	-583	-622	-865	563
	206	979	178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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55	889	369	788	167	646	534	25	-232	586	-179	-1287	-774	272	-683	-945	-161	-414	-460	-865	1207
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56	-404	369	-788	-99	1015	-238	-25	176	741	-189	-1287	122	-569	132	-945	-253	623	-622	-865	938
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
57	19	1986	-788	-318	-646	-238	-25	392	1278	-333	-1287	213	-569	-5	-171	-264	176	-622	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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58	-4	1498	-788	-641	-646	-238	1001	442	-165	-169	508	-774	-569	346	964	-7	-583	-78	-865	272
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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59	711	369	-788	-84	262	179	884	-1245	822	-170	621	-774	-569	-683	-945	-7	-22	22	-865	115
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
60	142	369	-788	663	451	-238	-25	-1245	-172	-3	-1287	213	-569	1051	-56	-664	189	80	-865	413
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
61	379	369	-788	-167	262	495	-25	-870	-172	255	-1287	-774	62	719	-945	319	289	-65	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	1329	-3313	-153	*	*											
62	717	1285	-788	63	-646	94	-25	-160	-159	-184	644	-675	-44	807	-945	-55	114	-87	-865	-707

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
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63	-170	369	-228	655	-646	301	-25	-1245	-172	-740	641	565	-569	-683	434	-383	533	673	-865	-707
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
64	138	369	-788	422	-646	-238	-25	-1245	-172	355	463	-774	-569	377	839	254	-414	374	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
65	-4	369	-547	-84	-646	417	-25	-394	-172	333	-1287	1241	-569	375	623	-664	-583	-622	-865	272
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
66	-404	1506	-788	310	-646	179	1034	-1245	768	-179	-1287	-774	-569	-3	-945	-264	189	346	-865	1258
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
67	333	369	-788	-962	-646	316	1117	-1245	-172	-740	-1287	849	-569	-683	501	285	543	68	865	845
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-70	-7794	-4535	-732	-1329	-3313	-153	*	*											
68	-378	1630	-762	-86	-619	333	285	-407	373	-714	535	1069	-543	172	924	-638	-557	61	-838	680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
69	802	396	67	-664	-619	-211	1	-925	-146	431	1256	9	-543	-656	534	-638	-557	367	-838	680
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-	122	7735	-3714	732	1329	-3346	-149	*	*											
71	331	443	-375	559	-329	390	1206	-433	799	-667	703	-701	655	-610	-872	366	-510	-549	791	-633
-	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	11	7627	8627	732	1329	3132	-175	*	*											
72	289	415	-742	-916	-600	597	21	-1199	-126	650	1291	28	-523	-637	-899	654	-537	68	-819	-661
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-	-11	-7691	-8691	-732	-1329	-3370	-147	*	*											
73	-341	415	172	-916	-600	225	21	-387	-126	623	1182	-706	-523	-637	88	-568	-537	640	-819	890
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-	-11	-7691	-8691	-732	-1329	-3370	-147	*	*											
74	-358	415	170	-916	-600	-192	21	-240	787	424	691	-489	109	44	-899	300	-537	-32	-819	559
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7691	-8691	-732	-1329	-3101	-179	*	*											
75	-385	388	-769	343	-627	-219	74	-1226	553	-160	950	585	-550	-664	1117	365	-564	-89	-846	-687
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7752	-8752	-732	-1329	-3339	-150	*	*											
76	-385	388	-769	1216	378	-219	-6	-1226	-153	-202	-1267	-755	-550	854	-926	300	-564	570	-846	550
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7752	-8752	-732	-1329	-3339	-150	*	*											
77	162	388	60	518	-627	-219	865	-1226	303	244	-1267	-755	-550	821	430	-645	-564	110	-846	306
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7752	-8752	-732	-1329	-3339	-150	*	*											
78	385	388	131	569	754	-219	-6	-235	-153	619	-1267	-755	-550	271	-926	12	-564	-390	-846	860
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	10	-7752	-8752	-732	-1329	3339	-150	*	*											

79	527	388	-769	260	311	115	1501	-155	797	-151	-1267	1	-550	-664	359	-645	-564	603	-846	-687
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80	-404	369	-788	320	369	-238	1034	-191	256	116	-1287	-774	-569	377	1028	-664	-583	544	865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
81	-404	2462	126	-962	-646	-238	1117	-985	366	6	889	-774	-569	375	95	198	-583	-622	865	520
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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82	-404	369	124	-285	119	241	-25	297	417	487	-1287	-774	-569	-683	34	226	-583	-106	-865	520
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
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83	250	369	13	-962	1137	-238	-25	680	-172	-228	-1287	-774	-569	132	41	343	-583	-184	865	564
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84	370	369	-788	-112	808	-238	1519	-1245	-172	109	1685	7	-569	-683	-945	-664	-583	74	865	756
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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86	148	1431	-788	-106	541	-238	-25	-985	740	54	-1287	-774	-569	345	-945	874	583	143	-865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-10	-7794	-8794	-732	1329	-3313	-153	*	*											
87	714	2092	-788	-962	-646	-238	-25	-1245	272	369	867	213	-569	-683	-945	848	-583	-622	-865	707
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
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91	142	2166	-93	-194	-646	-238	-25	545	-172	474	-707	577	-569	-683	-158	-664	-583	22	-865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
92	370	1530	-213	214	-646	-238	1001	-1245	191	436	-1287	659	-569	105	-945	-664	-583	495	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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94	458	369	-788	1045	814	-238	1481	583	-172	-740	-1287	-774	-569	352	-945	-664	164	-622	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
95	148	369	-788	-411	649	-238	873	278	908	-740	-1287	220	266	554	-945	-664	-414	92	-865	442
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
96	-404	369	-788	-632	-646	-238	1418	-1245	635	224	283	19	-569	-683	-51	406	457	91	865	530
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-	-90	-7794	-4153	-732	-1329	-3313	-153	*	*										
97	-369	404	-754	-927	868	-203	10	-1210	291	258	-1252	683	-535	-648	739	371	-71	381	830	672
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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98	232	444	-714	-887	458	-163	50	250	331	302	-1212	-700	-495	-608	-870	911	-509	488	-790	-632
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
-	-171	-7619	-3232	-732	-1329	-3397	-144	*	*										
99	294	507	-651	-824	-508	222	395	-1108	418	410	-1149	937	200	-545	-58	-115	-446	-485	-727	686
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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100	149	507	397	417	-508	14	113	-938	-34	415	-1149	358	-432	-545	-807	148	-446	-124	-727	684
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101	512	1452	-607	-137	-465	-57	467	-253	9	303	479	-593	-388	-27	216	191	-402	-441	684	-525
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-	-141	-7346	-3524	-732	-1329	-3502	-133	*	*										
102	238	2044	932	-736	581	-12	201	-1019	54	-514	-1060	655	-343	-457	-719	-438	396	-396	-638	-480
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-15	-7219	8219	732	-1329	-3540	-130	*	*										
103	160	1626	146	736	238	-12	1328	-1019	54	658	-482	-548	499	-457	-719	-438	-357	-396	-638	-480
-	206	979	-178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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104	178	596	562	69	420	-12	201	-1019	483	793	-1060	246	-343	-457	262	373	-357	-396	-638	480
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105	-178	1726	-562	381	-420	311	201	-167	266	42	-1060	411	-343	-457	30	-438	-357	247	-638	480
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106	-178	596	-562	-736	385	-12	201	-291	54	588	-1060	-548	-343	-457	-719	220	-357	1060	-638	-480
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107	-217	556	-602	-776	-459	-51	1075	444	14	403	471	407	-383	-496	-758	130	-397	486	-678	-520
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108	551	485	-673	421	-530	-122	91	-1130	-57	-625	1961	-8	328	-567	-80	115	-468	9	-749	-591
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-12	-7520	-8520	-732	-1329	-3442	-139	*	*										
109	49	1614	-525	-847	-530	-122	782	-1130	-57	-625	1207	-128	395	403	1000	-36	114	-507	-749	-591
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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110	162	450	135	-238	1269	-158	55	-1165	337	-230	-1206	-523	-489	-603	130	198	507	-542	-785	353
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111	507	409	-749	-279	875	-198	1148	-6	-133	-270	-1247	-735	622	-643	-905	385	216	-583	-825	155
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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112	632	369	97	-962	1599	94	-25	-1245	-172	-740	-1287	-774	774	-683	483	403	-583	-622	-865	-707

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
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113	-404	1994	-788	-962	-646	-238	1823	-1245	-172	101	-1287	-19	819	-683	420	-161	-583	346	1296	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
115	-67	667	-788	207	385	-238	-25	816	-172	118	-1287	-774	185	-683	-945	636	542	622	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
116	534	369	-788	261	383	-238	-25	-175	-172	217	-1287	-774	756	132	-945	486	-583	-106	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
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119	176	2168	506	-929	153	-205	8	487	440	431	337	-741	-536	-650	-912	-631	-73	589	-832	673
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7718	8718	-732	-1329	-3353	-149	*	*											
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121	610	403	755	-53	613	204	8	-857	-139	526	-1253	-741	-536	315	-912	-631	41	1104	832	-673
-	206	979	178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	-97
-	-10	7718	8718	-732	1329	-3353	-149	*	*											
122	-371	403	-755	938	741	-205	8	-157	-139	-136	-1253	-741	245	394	-912	-631	31	587	-832	320
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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123	-332	441	950	-890	364	-166	47	-900	-100	714	-1214	109	352	-611	-873	-79	-34	209	-793	-634
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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124	215	441	530	-890	441	-166	47	-361	-100	683	-1214	-702	-497	-611	-86	-592	-511	614	-793	515
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
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125	-306	462	-696	-870	385	-145	68	-1153	-80	670	-162	-682	-477	470	-852	880	281	-367	-772	623
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7579	-8579	-732	-1329	-3422	-141	*	*											
126	28	462	-696	-226	1020	-145	1201	-1153	744	-648	-1194	-682	386	468	-852	-160	101	-13	-772	535
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-	-82	-7579	-4313	-732	-1329	-2922	-204	*	*											
127	375	434	-723	-897	1226	-173	40	241	657	-675	-1221	-709	753	-618	-880	42	-182	-557	-800	595
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7645	-8645	-732	-1329	-1510	624	*	*											
128	-671	103	-1055	1229	445	-504	-291	-91	151	-1007	-1553	-1041	263	-121	-1211	1749	-96	-244	784	1167
	206	979	-178	-352	36	372	585	635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
	22	-8346	-6392	732	-1329	-2953	200	*	*											

129	-540	111	-1047	-52	643	-489	-283	-30	23	-999	-1545	-238	-828	-941	-1203	-362	2050	289	551	288
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-62	-8331	-4684	-732	-1329	-2973	-197	*	*											
130	-633	140	-1018	-395	154	-467	443	778	-402	-213	-1516	335	-799	-912	-765	1785	-813	-852	-1094	322
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131	-115	173	-276	-294	511	-435	-222	-1442	461	-592	-1483	-35	-766	2557	-1142	-758	-767	-174	-1061	350
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-	-7	-8216	-9216	-732	-1329	-2700	-241	*	*											
132	-504	139	-1019	-423	-876	-468	-255	-1476	196	-971	399	2438	-264	-913	-1175	-381	-722	1231	-1095	-937
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8280	-9280	-732	-1329	-3034	-188	*	*											
133	-634	139	-1019	-1192	-876	-51	-255	547	-403	1564	370	-1005	-264	-913	154	-716	-814	539	-1095	-937
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8280	-9280	-732	-1329	-2924	-204	*	*											
134	-643	131	2147	-321	905	-18	1242	205	-411	-979	-1525	-231	-808	-494	-264	-903	-230	-861	-1103	-945
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8295	-9295	-732	-1329	-3018	-190	*	*											
135	-643	131	494	424	-885	-477	-142	-1484	-411	-556	-1525	-324	28	-921	-188	1922	-822	-145	-1103	-613
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-41	-8295	-5326	-732	-1329	-3018	-190	*	*											
136	-82	451	1009	395	-867	1932	-246	-1107	53	-213	-1507	-995	-790	-903	-1166	-221	-791	655	-1085	-927
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	7	8263	9263	732	1329	2792	225	*	*											
137	231	126	681	149	-889	-481	-268	-398	-52	-983	-1530	-1017	-56	-926	1188	162	2257	308	-1108	-950
	206	979	178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	7	8304	9304	732	1329	3022	190	*	*											
138	301	126	2141	341	421	17	759	-402	-415	148	-1530	-259	-812	-926	-3	-660	-826	-865	-1108	-950
	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	7	8304	-9304	732	-1329	3022	-190	*	*											
139	-647	126	-334	-188	-230	460	-268	-1488	-415	1560	-1530	-1017	676	-926	-179	-230	-826	-865	-1108	166
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8304	-9304	-732	-1329	-2386	-306	*	*											
140	-706	67	-514	-384	-156	-540	700	-1547	-474	-480	310	-1076	-871	-985	82	2070	26	-924	771	-58
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8411	-9411	-732	-1329	-2916	-205	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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143	-706	67	-190	-1264	-948	13	-327	-1547	1029	-76	207	-282	358	-985	-1247	-543	-712	-388	4036	-1008
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8411	-9411	-732	-1329	-2660	-248	*	*											
144	-176	51	-1107	-1281	939	-556	-343	2019	-491	-488	303	-1093	-888	-1001	65	-307	-154	603	-1183	-1025
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
145	-180	51	-1107	-615	-964	-556	1162	-203	48	1466	-1605	-1093	768	-1001	-252	-309	-902	228	-1183	-1025
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	164	41	-73	-335	-54	27	-12	-255	-97

-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
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-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
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151	-237	925	-399	556	486	-556	814	104	2013	12	-1605	-1093	-888	-1001	-1263	-983	-902	-502	1183	-1025
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152	1688	51	-403	675	-160	159	-343	-509	-317	-488	-1605	25	-888	386	-1263	-497	-148	-941	-1183	-1025
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153	-324	51	-305	110	2422	-556	-343	-398	-491	-153	-1605	363	-348	-36	-1263	-154	-902	-109	-1183	31
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	6	8440	-9440	-732	-1329	-2839	-217	*	*											
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	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
	-6	8440	-9440	-732	-1329	-2839	-217	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
156	-723	1080	-1107	489	579	-556	-343	-712	-491	-98	-1605	-1093	-888	-1001	-489	-65	-424	-250	-1183	2849
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
157	-723	51	-523	858	-964	-556	398	-1564	2013	-1059	1219	-1093	-888	59	496	89	-902	-941	-1183	707
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158	51	51	-531	-512	939	-556	782	-476	93	-546	-34	-1093	-888	56	-1263	25	-902	1827	-1183	-1025
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-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
159	-218	51	-1107	-431	-160	-556	528	2263	-491	-86	-250	-1093	-888	-213	-1263	-983	-902	-319	1602	451
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
161	-723	51	-1107	123	-964	-556	555	-753	1023	-1059	-1605	-1093	-888	-1001	-1263	1825	301	232	1101	-1025
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	-6	8440	-9440	732	1329	-2839	-217	*	*											
162	-300	51	1107	-1281	2422	207	1100	420	-491	138	-1605	441	-888	-1001	-1263	-309	-142	-941	-1183	-1025

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
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164	-162	351	-1107	-731	-964	-140	-343	-753	2013	-651	-1605	427	-888	-1001	160	416	902	118	1127	-1025
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-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
165	1797	952	-1107	-431	144	-556	-343	-1564	-491	-273	-74	-299	-888	-67	84	33	-653	314	1123	1025
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-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
166	-171	805	-1107	1918	-964	-556	1290	488	-491	105	-1605	-745	-888	-1001	-1263	-983	-131	-425	1183	591
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-94	-8440	-4051	-732	-1329	-2839	-217	*	*											
167	-675	99	-336	342	-917	1675	603	-1516	392	-449	-1557	891	-840	-954	55	-935	134	-893	1026	-977
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8354	-9354	-732	-1329	-2937	-202	*	*											
168	-234	99	-772	468	-917	-509	1445	-1516	-443	-1011	-1557	2246	-840	-954	554	439	854	-796	1149	977
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-	-7	-8354	-9354	-732	-1329	-2937	-202	*	*											
169	248	99	-1059	975	-917	-509	830	-678	-443	1423	-1557	-1045	-840	-19	-572	-261	-100	-893	1136	-977
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-	-100	-8354	-3965	-732	-1329	-2937	-202	*	*											
170	365	148	444	-983	-867	-55	246	-106	36	550	809	-996	-342	-904	-1166	-885	1865	-844	-1086	-928
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-533	-8261	-1710	-732	-1329	-178	-3106	*	*											
171	-1053	599	-1437	2679	-1295	-453	388	-1038	-821	-142	-574	-340	-371	-538	-744	-965	-1232	-1271	806	-1355
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9006	-10006	-732	-1329	-1974	-424	*	*											
172	-547	-279	-632	-38	-1295	-887	472	-1894	-366	2282	-1935	-1423	-1218	-1332	-600	-317	-1232	-1271	796	-1355
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-	-4	-9006	-10006	-732	-1329	-1444	-661	*	*											
173	-128	450	-1475	-239	-1332	-924	319	-1931	2734	-570	927	-178	-1255	-1369	-1631	-104	-769	-1308	-1551	-1393
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9064	-10064	-732	-1329	-1801	-488	*	*											
174	68	-317	-1475	-795	-1332	-924	-711	-90	-858	157	-1973	-1460	-1255	-1369	3030	-586	-1269	-1308	-1551	-1393
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9064	-10064	-732	-1329	-1801	-488	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9064	-10064	-732	-1329	-1801	-488	*	*											
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-	-37	-9064	-5398	-732	-1329	-1801	-488	*	*											
177	-506	625	-1453	-1626	-1310	-902	451	-636	-315	-35	-1951	3086	-1234	-664	-612	-312	-1248	-350	-1529	-1371
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-	-42	-9030	-5215	-732	-1329	-1907	-448	*	*											
178	-478	-271	-729	217	-1286	-878	-665	-1885	214	-422	-1926	-1414	-1209	-529	-1585	2576	-547	-1262	-1505	-1347
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-32	-8992	-5649	732	1329	-2015	410	*	*											

179	-464	-253	-831	-731	-1268	-860	1667	-1867	-273	2152	-1909	207	-1192	-13[illegible]	-174	-780	1206	-1244	-1487	-991
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-8965	-9965	-732	-1329	-2087	-387	*	*											
180	-1026	1326	-1411	2661	-497	-860	-647	-1867	-328	-378	-1909	-377	-534	-1305	-565	295	-1206	1244	-1487	-1329
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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181	-1000	-227	-1385	2820	-1242	-834	-621	-986	-768	-474	8	-68	-63	-1279	-530	-771	1180	-1218	-1461	-1303
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-	-46	-8924	-5082	-732	-1329	-2186	-358	*	*											
182	-430	-201	-1358	-669	-420	-808	979	-1815	-742	-560	-259	-1344	-1139	3384	-496	-499	-1153	-1192	-1435	-1277
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8882	-8061	-732	-1329	-2277	-333	*	*											
183	-972	593	-656	-253	-551	-805	-592	2968	-740	-1308	-1854	-1342	-1137	-1250	-171	-1231	-1151	-1190	1594	-1274
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8878	-9878	-732	-1329	-2285	-331	*	*											
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-	-5	-8878	-9878	-732	-1329	-2285	-331	*	*											
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-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
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-	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	-5	-8878	-9878	-732	-1329	-2285	-331	*	*											
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192	21	-179	-1337	-648	-1195	2677	-574	-1794	-721	-1289	-1835	-1323	-449	-1232	-217	313	-1132	-1171	-1414	-1255
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-	-52	-8714	-4927	-732	-1329	-2567	-267	*	*											
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-	-5	-8668	-9668	-732	-1329	-2634	-253	*	*											
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-	-5	-8668	-9668	-732	-1329	-2634	-253	*	*											
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-	-1895	-8668	-457	-732	-1329	-2634	-253	*	*											
200	-31	743	-415	-589	127	136	349	-872	201	-367	-913	-401	-196	-309	-571	713	-210	-249	2699	93
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-	-20	-6747	-7747	-732	-1329	-3653	-119	*	*											
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202	135	793	344	-539	-222	186	398	-822	273	28	1395	-351	-146	-259	76	-241	-160	199	441	283
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-23	-6560	-7560	-732	-1329	-3688	-117	*	*											
203	19	793	365	-539	-222	186	398	755	251	-199	-863	-351	-146	-259	267	-241	160	319	441	283
-	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	352	6560	2278	732	1329	3688	117	*	*											
204	495	868	290	464	148	260	725	747	538	-242	-788	-276	-71	-151	398	-166	-85	-124	366	208
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	29	6236	7236	732	1329	3735	113	*	*											
205	197	868	270	464	148	260	473	747	326	-242	-788	-276	-71	496	-447	321	-85	104	366	208
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206	495	868	-290	-464	-148	260	473	-747	326	-242	-788	357	196	-184	-447	70	93	-124	-366	208
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-	-29	-6236	-7236	-732	-1329	-3735	-113	*	*											
207	210	868	-290	72	-148	260	473	-747	414	-242	-788	-276	-71	606	80	-166	-85	-124	366	208
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-	-220	-6236	-2961	-732	-1329	-3735	-113	*	*											
208	132	905	-116	30	-110	298	511	-709	364	-204	-750	554	-33	-147	-409	-128	-47	-86	-329	171
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-59	-6047	-5326	-732	-1329	-3757	-111	*	*											
209	137	910	-247	-421	-105	303	516	-704	385	-199	-745	-233	-28	-142	717	-123	-42	-81	-324	-166
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
-	*	*	*	*	*	*	*	*	0											

//

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NAME domb.txt
DESC
LENG  132
ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:44:31 1999
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NULT       -4  -8455
NULE      595  -1558     85    338    -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y
          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
         -2829      *   -219
      1     81    256   -902  -1075   -759   -351   -138    -75    687   1392  -1400   -887   -683    323   -407    403   -696   -735   -978   -820
      .    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -8  -8054   9054   -732  -1329  -3255   -160  -2829      *
      2    444   1482   -498  -1075    462   -351   -138  -1358   -285   1374  -1400    279    250   -796  -1058   -777   -696   -735   -978    500
      .    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -   -102  -8054  -3948   -732  -1329  -2863   -213      *      *
      3   -507    267    225  -1065    472    340   -128  -1348    -17   -156  -1389   -877   -672    147   -325   1476    686    220   -968    169
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27     12   -255     97
      -     -8  -8030   9030   -732  -1329  -2809   -222      *      *
      4    406    223    935   1780   -792   -384   -171  -1392    213    -53  -1433   -921   -716   -829    235    173    259    648   1011    853
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335     54     27     12    255     97
      -     -8   8119   9119   -732  -1329  -2769   -229      *      *
      5   -446    182    975   1149    129   -425   2716  -1432    370    153  -1473   -505   -756    249    460    407    486    809   1052    894
      .    206    979    178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27     12    255     97
      .    -32  -8200   5758   -732  -1329  -2867   -213      *      *
      6   -600    174    984  -1158   -842    -76   -221    461   -368     39  -1482    821   1664   -878    335   -537    565   -818  -1060    273
      .    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     99  -8217  -3995    732  -1329  -2957   -199      *      *
      7   -566    207    951   1619   -808   -400   1532   -643    220   -207  -1449   -936   -492   -845    715    -17    359   -784  -1027   -869
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      -     -8  -8150   9150   -732  -1329  -2686   -244      *      *
      8   -612    162    100    -97   -854   -446   -233   -250   1080   1455  -1494   -982   -777   -147    -85   -872   -210   -830  -1073   -914
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -7  -8240  -9240   -732  -1329  -3095   -180      *      *
      9   -315   1386   -996   1286    289   -446   -233    162   -380    742  -1494   -982   -777   -581   -213   -318   -791    355  -1073   -914
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -7  -8240  -9240   -732  -1329  -3095   -180      *      *
     10     73   1537   -996   -241    989   -446   2695   -558   -380   -257  -1494   -982   -777   -891    283   -872   -791   -830   1462    995
      -    206    979   -178    352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -7  -8240  -9240   -732  -1329  -3095   -180      *      *
     11     73    162    996   1170   1314   -446   -233   1629   -133   -948  -1494     94   -777   -891    969   -115    104   -830  -1073   -914
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      -     -7  -8240   9240   -732  -1329  -3095   -180      *      *
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	206	979	-178	352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	12	-255	97
	7	8240	-9240	-732	1329	3095	180	*	*											
13	94	162	996	1170	908	446	-233	467	501	368	1494	982	777	-891	581	872	791	830	3489	-914
	206	979	178	352	-36	372	585	-635	438	-130	677	-164	41	-73	335	-54	27	12	255	97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	3095	-180	*	*											
15	-612	696	-996	-241	326	-446	-233	-162	295	1172	-1494	-982	-777	228	45	-369	422	135	-1073	-914
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-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
17	22	162	100	-788	703	-446	1210	-1453	-380	924	-1494	-982	136	1877	-755	-872	-791	-830	-1073	-720
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-95	-8240	-4052	-732	-1329	-3095	-180	*	*											
18	318	1574	-952	843	-347	-401	2740	-1409	-336	-121	-1450	12	-80	-846	-1108	-827	-277	44	-1028	-870
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8152	-9152	-732	-1329	-2694	-242	*	*											
19	497	162	-301	484	394	-304	1087	-250	-380	-340	-1494	-982	-777	228	-1153	-872	1719	-830	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
20	-118	1485	-996	-241	-854	-377	-233	-688	-380	1427	-1494	-982	-777	228	641	-578	160	-830	-167	-194
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
21	612	1249	-996	-505	-854	-446	988	-250	-270	-22	-1494	-982	217	1877	649	-872	29	526	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-94	-8240	-4063	-732	-1329	-3095	-180	*	*											
22	-568	206	100	-310	-810	-402	344	133	398	-904	-1450	1762	-80	-847	971	-828	73	98	-1028	-870
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8153	-9153	-732	-1329	-3161	-171	*	*											
23	-568	740	-952	1330	-810	-402	1205	-109	398	826	-1346	192	-733	-847	243	-828	-747	-786	-1028	-870
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-8	-8153	-9153	-732	-1329	-2697	-242	*	*											
24	-612	1559	-996	-1170	235	-446	-46	240	-380	55	646	-99	-403	793	-298	-745	-791	-830	1324	2161
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
25	-612	2167	330	1286	235	-446	-233	-1453	418	-146	-1494	-982	279	-891	-1153	-745	199	-830	2074	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
26	-612	986	700	-192	-854	-446	-233	-1453	-380	1455	-1494	94	-777	-891	-1153	-248	476	32	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
27	-612	2265	996	574	311	-446	-233	-1453	-380	38	2600	-982	-777	-891	1017	-872	-321	-830	-1073	-914
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
28	-371	162	430	-1047	819	-446	2074	-1335	-133	-704	740	-982	-777	938	1668	-562	-762	-29	-1073	-914
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-86	-8240	-4201	-732	-1329	-3095	-180	*	*											

29	572	201	1643	48	-814	406	1028	130	733	-240	1454	-942	65	-36	-232	-705	178	-790	-1033	875
	206	979	-178	-352	-36	372	585	-635	438	-130	677	164	41	-73	-335	54	27	12	-255	97
-	51	8161	-5004	-732	-1329	-3156	-172	*	*											
30	550	223	1134	392	436	-384	727	-1392	-319	-100	1433	-921	-716	-829	1674	-810	90	-337	-1011	853
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-63	8119	-4672	-732	-1329	-2769	-229	*	*											
31	-565	209	-171	-1123	-806	-398	2824	-1406	-333	235	-1447	-935	-730	1402	755	-3	-162	-783	-1025	-867
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8149	-9149	-732	-1329	-2650	-250	*	*											
32	-612	1445	-996	-354	-854	-446	1160	92	-380	1440	-1494	-982	-746	617	-1153	-91	-791	213	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
33	-612	162	1655	-927	-854	-446	852	419	-380	277	-156	93	-777	-76	-1153	-311	-791	-29	-1073	946
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
34	612	511	347	353	-854	-119	424	-438	-380	132	-35	790	-777	2213	-1153	-872	-791	-830	-1073	-914
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	485	8240	-1826	-732	-1329	-1815	-482	*	*											
35	240	2643	-958	71	-815	-407	-194	1517	-341	-674	-1456	-943	-249	1029	-1114	-833	-752	70	-1034	444
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8167	9167	-732	-1329	-2817	-221	*	*											
36	58	1399	-848	362	379	-433	-220	-1441	-212	-75	2431	-970	-765	-135	-507	-357	671	-818	1138	-902
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
37	-268	174	-984	703	358	-433	-220	-1441	361	854	2431	-970	-716	-878	-1140	-859	385	818	1060	902
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	255	97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
38	-599	3109	-984	-223	-841	-433	-220	-1441	-12	672	530	-970	-525	374	435	-859	779	818	1060	1161
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	-12	-255	97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
39	370	1571	984	-913	120	157	98	484	-87	-936	1237	-970	-638	-655	496	1247	-779	-17	-1060	902
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	7	-8215	9215	-732	-1329	-3111	-177	*	*											
40	103	174	17	-1157	-379	-433	-220	-1183	128	-192	2983	-970	-765	485	-367	-681	-779	324	-1060	479
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
41	465	916	479	-109	406	-433	864	-26	-368	-936	-1482	160	-765	-878	-74	-859	-779	-818	-1060	2315
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
42	-599	174	-984	-1157	-841	1307	1001	-948	758	-936	-1482	-258	-765	374	451	-859	-62	-17	2111	597
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
43	-599	174	-984	-1157	301	-433	1676	1578	-368	39	-469	-970	-765	374	-1140	-455	143	702	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
44	-370	3425	-17	-1157	-120	-433	-220	-1121	308	360	753	-970	-765	110	-1140	-859	687	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
45	103	174	479	-1157	720	-433	-220	-1441	1868	-831	-1482	-20	-765	1322	-1140	-859	150	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

	7	-8215	9215	-732	-1329	3111	-177	*	*										
46	599	174	418	701	-841	433	220	373	380	165	1482	-970	765	1237	1140	859	-779	1332	1060	902
	206	979	-178	-352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	255	97
	-7	-8215	9215	-732	-1329	3111	-177	*	*											
47	-599	174	984	388	818	-433	665	-128	1471	194	530	-970	-765	-878	-1140	-859	-449	66	-1060	688
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
48	-599	174	-984	291	379	-433	-220	-1441	-121	506	1103	1646	-765	-878	17	-395	562	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
49	-599	1398	-352	-776	-841	-433	-220	1435	380	145	1237	237	-765	295	-1140	-859	613	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	9215	-732	-1329	-3111	-177	*	*											
50	-599	1965	1456	131	920	-433	-220	-918	-368	-936	347	-970	-765	882	368	-143	-569	-483	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
51	90	174	-984	-84	-841	-433	1508	-1441	-368	843	530	-61	-765	973	618	-357	85	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-7	-8215	9215	-732	-1329	-3111	-177	*	*											
52	-599	1163	208	648	-841	-433	-220	516	1471	-936	87	-970	-765	-878	84	-859	553	-818	-1060	417
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
53	-599	174	106	-1157	1880	156	-220	-294	-368	-292	-1482	-970	-96	-878	515	-766	791	-818	-1060	1183
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
54	-599	174	-567	-213	999	-25	864	-295	1471	128	659	-970	-765	594	-1140	-859	-779	50	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	7	8215	-9215	-732	-1329	-3111	-177	*	*											
55	-599	1398	984	-776	672	-433	-220	1563	333	540	725	106	-765	402	-1140	-859	-779	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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56	90	1074	133	-84	306	-433	-220	1641	270	-936	888	751	-765	-878	-1140	-75	-779	-818	-1060	-902
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-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
57	-599	174	-984	-1157	-841	-433	-220	-129	876	-240	756	-258	-765	110	225	-859	-779	1474	-1060	1161
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
58	-599	1541	497	-1157	-841	-433	1060	-426	833	-936	753	-970	-765	-878	376	-859	1405	367	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	9215	-732	-1329	-3111	-177	*	*											
59	1158	1541	-984	-1157	-841	-433	601	-238	661	-936	347	775	-765	-878	912	-578	156	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
60	-599	174	34	-228	-841	-433	1586	-295	366	-240	924	-190	-765	332	-1140	-23	-779	-818	-1060	2174
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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61	-300	963	-315	-402	-1141	-733	308	1827	1169	-225	-1781	-1269	-69	-4	-985	-1159	-1078	-582	-1360	999
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8756	-9756	-732	-1329	-2548	-271	*	*											
62	-899	-125	1890	-1457	-1141	-57	-520	-1740	-667	-173	3033	-810	-1064	882	-215	-534	-1078	-1117	-1360	-1201

	206	979	178	352	36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	-255	97
	5	-8756	9756	732	1329	2548	-271	*	*											
63	241	1101	1283	1457	1141	733	-520	-536	-28	790	3158	-34	-1064	693	335	1159	-1078	-255	-1360	1201
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	73	335	-54	27	12	-255	97
	-5	-8756	9756	-732	-1329	2548	-271	*	*											
64	214	3570	-1283	1457	52	733	-520	-219	-28	-261	-1781	38	1364	103	-665	-337	-1078	-1117	-1360	-25
-	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8756	9756	-732	1329	2548	-271	*	*											
65	-899	1159	1283	1457	479	-221	2319	-1416	480	-256	-532	-1269	504	-697	-1440	1743	-1078	-1117	-1360	-1201
	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8756	-9756	-732	-1329	-2548	-271	*	*											
66	928	1559	-1283	-527	-1141	733	801	-45	-222	-696	3191	-1269	-1064	758	-1440	-1159	-1078	-255	-1360	-1201
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8756	-9756	-732	-1329	-2548	-271	*	*											
67	-196	2696	-1283	-1457	-1141	-733	-520	-593	-667	-591	-1781	161	-1064	-1178	-1440	-1159	-496	1386	-1360	2644
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8756	-9756	-732	-1329	-2548	-271	*	*											
68	-314	620	1283	-1457	-51	1731	-520	-46	-112	-851	-1781	-34	-1064	1784	-1440	-565	-1078	-358	-1360	899
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8756	9756	-732	-1329	-2548	-271	*	*											
69	-899	-125	-1283	915	-653	-107	17	1915	-667	-539	803	-1269	-1064	-1178	-282	123	-258	135	-1360	-298
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-257	-8756	-2636	-732	-1329	-1152	-862	*	*											
70	-320	3550	-1303	-428	-510	381	854	-1760	-132	-1255	-1801	-1289	-1084	-1197	-255	300	1236	-154	-1379	431
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
71	7	1230	1303	-1477	1636	-470	540	-223	1891	-559	-1801	-338	-1084	-1197	-1460	-1179	-1098	735	1379	365
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
72	541	-145	-1303	-1477	-1161	-753	-540	-86	1662	-586	-65	-1289	-1084	-1197	-1005	-1179	-169	1708	-1379	1665
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	9789	-732	-1329	-2498	-281	*	*											
73	-439	542	162	-1477	60	-753	-540	-457	2048	-586	-459	-1289	-1084	-1197	1777	-894	-1098	-336	-1379	-1221
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	8789	-9789	-732	-1329	-2498	-281	*	*											
74	-919	1139	-1303	-810	-1161	-162	-540	-1760	685	-279	-1801	2157	-1084	-1197	-125	-342	-163	1267	-1379	-1221
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75	-814	685	-1303	-428	-1161	-753	-540	1879	-132	846	-1801	-1289	-170	671	-1460	65	-1098	315	-1379	-1221
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-	-5	-8789	9789	-732	-1329	-2498	-281	*	*											
76	-919	-145	1951	-465	-198	-753	682	1385	-233	-3	-1801	-647	310	-448	-1460	-461	-431	-1137	-1379	-1221
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-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
77	-306	-145	-1303	307	-1161	-753	-540	-1760	1642	1604	-1801	-156	-1084	63	-243	-1179	-1098	-1137	-1379	-1221
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-	-5	-8789	9789	-732	-1329	-2498	-281	*	*											
78	-229	-145	-1303	1368	-1161	-753	683	-470	2047	-610	-1801	-82	-1084	-1197	-302	-553	-516	-316	-1379	-1221
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79	919	-145	-284	1202	2307	-104	-540	-744	-687	-870	1801	309	-1084	-79	-255	-100	-233	-377	-1379	-1221
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80	-919	-145	-251	1540	-17	-162	-540	-1760	1936	-945	-459	-1289	-841	-382	-899	-80	-1098	-474	-1379	248
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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81	-919	-145	1303	-48	-434	753	-540	1947	216	-363	-1801	-1289	-1084	63	53	-840	326	-1137	-1379	1933
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
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84	-234	-145	-61	-644	602	-753	-540	1298	185	-455	-1801	-748	-1084	1544	306	-1179	1017	-1137	-1379	-1221
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88	-351	622	1142	-1324	240	-600	698	86	573	-1102	-1649	-1136	100	-376	-1307	730	-945	320	1227	2294
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89	-248	7	-1150	248	81	-600	-387	-1607	455	549	-1649	1718	-931	-1045	222	-1026	-945	-984	-1227	1811
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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90	-766	7	-1150	467	-1008	80	-387	-1607	115	-1102	-1649	98	1272	-1045	72	1113	-615	968	-1227	-1069
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91	-51	89	-859	599	294	196	1392	-1032	282	-1021	-1567	-361	64	26	-1225	-944	296	1319	-1145	-987
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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92	232	149	-1008	-366	1934	-458	-245	-1465	-392	-664	-1506	-355	-789	1139	656	-68	-803	41	-1085	657
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93	-26	1433	-42	-1182	-866	-458	-245	-1465	-392	-960	2588	-994	553	-159	40	-68	6	164	-1085	998
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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97	111	4	1154	-718	1798	73	-390	-771	1605	496	-1652	-841	935	-438	1310	455	949	963	1230	1072
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	-255	-97
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	65	-8536	4588	-732	-1329	-2851	-215	*	*											
99	-736	37	-1120	-1294	491	-570	-357	-560	197	-1072	-1618	1672	-901	-1015	1498	700	-124	-215	-1197	283
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	6	-8476	-9476	-732	-1329	-2917	-205	*	*											
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101	6	76	-1082	-438	-939	-531	1046	-335	-145	1777	-1580	-284	-863	-976	-198	56	-877	-916	-1158	-1000
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102	698	76	-1082	12	-939	-531	-21	1494	-217	-46	-1580	-1068	-863	1870	-858	-384	-877	413	-1158	383
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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103	-698	76	-1082	-438	150	145	-318	-335	1751	-1034	-1580	-1068	-863	-976	-602	-957	-877	364	-1158	2364
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	420	-8407	-2002	-732	-1329	-2986	-195	*	*											
104	487	286	-872	1498	244	305	-108	321	-255	87	645	-857	-652	-766	-1028	-747	666	-705	-948	1243
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	-117	-7988	-3761	-732	-1329	-3275	-157	*	*											
105	-437	336	31	1547	-679	98	-58	600	-205	-530	252	-807	-603	750	-978	61	-617	-655	-898	-740
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-9	-7880	-8880	-732	-1329	-3334	-151	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-9	-7880	-8880	-732	-1329	-3334	-151	*	*											
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	-34	-7880	5714	-732	-1329	-3334	-151	*	*											
110	-426	347	-810	65	349	366	249	1634	-194	-762	-1308	281	-591	-705	-384	-686	309	-17	-887	-340
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-9	-7858	-8858	-732	-1329	-3360	-148	*	*											
111	-426	347	173	-984	-668	-99	-47	2054	-37	-762	-1308	77	-591	-705	-967	-578	-605	473	-887	449
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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112	-426	347	203	-984	554	-260	-47	658	-194	-153	-1308	156	-591	-705	-967	-253	-605	1585	-887	-729

-	206	979	-178	352	36	372	585	-635	438	-130	-677	-164	41	-73	335	54	27	-12	-255	-97
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113	178	595	-562	736	-420	12	201	604	54	93	-1060	-548	-343	661	719	186	507	466	-639	481
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-	-15	-7218	-8218	-732	-1329	-2162	-365	*	*											
114	-422	351	-807	-980	480	-256	-43	248	-190	-759	-1305	-793	445	116	-963	682	-70	23	-883	2663
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-	-106	-7851	-3904	-732	-1329	-3370	-147	*	*											
115	306	393	-764	-938	761	-214	351	-1221	418	-716	-1262	2036	-545	-659	-921	-640	-559	-205	-841	1159
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-77	-7755	-4407	-732	-1329	3414	-142	*	*											
116	334	422	-736	-910	509	-185	28	-1193	-120	-688	600	410	-517	-630	-892	1534	-531	-570	-812	742
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7688	-8688	732	-1329	-3443	-139	*	*											
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	11	7688	-8688	-732	-1329	3443	-139	*	*											
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	141	7688	-3506	-732	-1329	-3443	-139	*	*											
122	336	475	-683	-857	-540	-132	81	-1140	-67	1288	66	284	135	-577	-202	-558	-478	-41	-759	601
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	12	-7558	-8558	-732	-1329	-3492	134	*	*											
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-	-12	-7558	8558	-732	-1329	-3492	-134	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-175	-7558	3196	-732	-1329	-3492	-134	*	*											
127	-236	538	-620	-794	252	-70	143	-1077	-4	1551	-1118	-606	-401	-200	-776	-90	-109	-454	-696	-538
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-13	-7396	-8396	-732	-1329	-3548	-129	*	*											
128	-236	538	-620	-794	233	-70	400	-1077	-4	-186	-1118	-182	-401	2338	-776	-496	-415	349	-696	-538
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-	-159	-7396	-3347	-732	-1329	-3548	-129	*	*											

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	206	979	178	352	35	372	585	635	438	-130	677	-164	41	73	335	54	27	12	255	51			
-	1279	-7250	783	732	1329	3590	-125	*	*		*												
130	143	917	-241	-415	99	309	522	-377	375	305	739	-227	-22	-135	397	117	36	75	-317	159			
-	206	979	-178	352	36	372	585	-635	438	-130	-677	-164	41	-73	335	-54	27	-12	-255	97			
-	-35	-5970	6970	732	1329	3802	-107	*	*														
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-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*			
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        -3849      *   -104
     1  -1243   3362    377   -175  -1846    233   -224   -705  -1396  -1082  -1804    483   1754   -133   -496   -440   -411   -860  -2921  -1398
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -41 -15580  -5155   -732  -1329  -2028   -406  -3849      *
     2  -1097   4294    273   -591  -1829    190   -179   -883  -1847  -1201  -2130    848   -397    184  -1066   -631  -1083   -615  -1242  -1474
     -    179   1091   -143   -347    -57    372    595   -649    412   -146   -690   -126     62    -41   -333    -46      8    -37   -289   -109
     -  -7046    -33  -6071     -1 -11285  -2558   -268      *      *
     3  -1144   3490     86   -180  -1019    515   1204  -1205  -1645  -1856  -2683   1848   -622   -122   -240   -394   -507  -1185  -1847   -943
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -70 -15619  -4409   -732  -1329  -2833   -218      *      *
     4  -1063   2786      8   -549  -2315   1697    717  -1290  -1426  -1312  -1821    786    463    371     54   -346   -333  -1609  -3656   -913
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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     5   -469   3330   -240   -170  -1205   1710    261  -1770  -1747  -2058  -3115    949     19   -446  -1204   -369   -137  -1083  -1903  -1211
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     -    -38 -15616  -5259   -732  -1329  -1892   -453      *      *
     6  -1119   3210   -349   -267  -1044    926    380   -898   -817  -1515  -1938      6    104    -71    259   -299    830   -260  -3057   -977
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     -    -43 -15652  -5077   -732  -1329  -2136   -373      *      *
     7   -964   4380   -351   -862   -856    499   -143  -1459  -1531  -1602  -2239    347     19   -258   -649   -851   -426   -772  -2438   -885
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     -  -6428    -48  -5583     -1 -11338  -2576   -265      *      *
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-15759	-8989	-732	-1329	-2777	-227	*	*											
13	-1081	3284	561	-56	-460	247	-189	-1946	-653	-858	-1334	415	1136	-133	-34	-447	-379	-1087	-866	-338
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	-11	-15771	-6995	-732	-1329	-3356	-148	*	*											
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26	-892	3343	44	-401	-1047	563	936	-1493	-1080	-1405	-1627	1051	810	-84	-26	69	-383	-1705	-1721	-926
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-	-102	-14586	-3870	-732	-1329	-7202	-10	*	*											
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-	196	1001	-170	-346	-43	371	577	-641	437	-138	-685	-167	51	-68	-320	-49	37	-22	-271	-102
-	-8766	-197	-2999	-2	-9612	-9492	-2	*	*											
45	-2278	3752	515	-1715	-921	1515	780	-2365	-1664	-1011	-2693	668	-1542	-427	424	-679	77	-3386	-1821	-574
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-379	-13798	-2115	-732	-1329	-9355	-2	*	*											
46	-2047	4754	251	-1869	-1678	-2942	183	-3041	-1113	-1366	-3464	359	-661	-1215	659	-532	-561	-1574	-2984	-482
-	200	1010	-181	-357	-40	366	589	-641	432	-134	-682	-160	34	-73	-324	-39	33	-17	-259	-95
-	-7524	-852	-1182	-9	-7395	-9794	-2	*	*											
47	-3156	5631	-3540	-3714	-3398	-2990	-2777	-3997	-2924	-3492	-4038	-3526	-598	-3435	-3697	-2177	-786	-3374	-3617	-3459
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
-	*	*	*	*	*	*	*	*	0											

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RF    no
CS    no
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NSEQ  0
DATE  Mon Mar  8 11:45:02 1999
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NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
         -2869      *   -212
      1  -1711   -938    252  -2269    791   -530   1782  -2553   -255    400  -2594  -2082   1076  -1990    956    -58   -842   1319  -2172   -813
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -    -15  -9930  -6763   -732  -1329  -3342   -150  -2869      *
      2  -1680  -1012    444  -2343    337    794    659    -95    267     56     11  -2156    548  -2064   1150    410  -1787    360  -2246   -276
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -    -39 -10024  -5267   -732  -1329  -2044   -401      *      *
      3   -993  -1219  -2377  -2551      6     23    386    294    149    143  -2875  -2363   1471  -2271   2148    152  -2172     44  -2453  -2295
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -    -27 -10282  -5810   -732  -1329  -3178   -169      *      *
      4  -2026  -1252  -2410  -2584     40    495  -1646    738    506  -1034  -2908   -486   2035  -2304    -97    417   -783   1205  -2486  -2328
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -    -44 -10322  -5089   -732  -1329  -3734   -113      *      *
      5   -627  -1238  -2396  -1057   -206    477  -1632    420    377    197  -2894   -511   1099  -2290  -2552   -982    -66   1920  -2472  -2314
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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      6  -1984  -1210   -662   -944   -500     22  -1604    375     63    558  -2866   -549    -36  -2262  -2524   -707    749   1923  -2444    223
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      -    -104 -10270  -3868   -732  -1329  -4011    -92      *      *
      7   -886  -1139    118  -2470   1076    866  -1533    249   -467   1467   -360  -2282    404  -2191  -2453   -165    181   -549  -2373  -2215
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      -    -29 -10181  -5714   -732  -1329  -2542   -272      *      *
      8   -905   -515   -840  -2578    692    629    469    825   -127    412    323  -2390    462  -2299  -1000    591   -568    976  -2481  -2323
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      -     -2 -10316 -11316   -732  -1329  -3192   -167      *      *
      9    417  -1297    570  -2629   -395   2129  -1692  -1011    -62   -869    271  -2441    922  -2350   -714    215  -2250   -233  -2532  -2373
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      -    -39 -10378  -5274   -732  -1329  -2733   -235      *      *
     10   -413  -1342   -319     84   -632    419   1786   -994    650   -553    224   -913   1755   -318   -454    410  -1245  -1116  -2576  -2418
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-	-92	-10432	-4028	-732	-1329	-2751	-232	*	*										
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-	-236	-10423	-2734	-732	-1329	-4142	-84	*	*										
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-	-80	-10189	-4228	-732	-1329	-2560	-268	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10274	-11274	-732	-1329	-2899	-208	*	*										
14	58	710	127	1315	479	941	369	-731	939	-950	59	-627	-318	-629	-589	-1590	-431	-870	-2523	-2365
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10369	-11369	-732	-1329	-1799	-489	*	*										
15	-451	-1464	952	-271	-2479	-1144	-1858	-3078	-320	-410	83	-231	77	963	-143	-287	1449	803	-2698	389
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-	-1	-10578	-11578	-732	-1329	-2637	-253	*	*										
16	-592	-1512	1475	-1458	1056	-2120	754	-818	712	-283	446	-2656	1396	-2565	-301	-1444	842	-269	-2746	-348
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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17	408	-1512	420	-1153	-939	767	764	608	-599	418	2180	-2656	-774	-507	94	-565	-784	-1001	-2746	-390
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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19	-1030	-1512	1215	377	465	-853	313	207	172	-1336	-1234	-337	-76	1488	1103	-874	-47	-1242	-2746	-755
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-	-35	-10541	-5436	-732	-1329	-3914	-99	*	*										
25	-2178	-1405	697	236	1989	-750	-913	27	-81	-891	-3060	-1030	277	234	418	-302	-2357	815	-1962	593
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-	-14	-10507	-6811	-732	-1329	-2264	-337	*	*										

26	-699	630	-642	-115	727	-948	1109	-3098	864	370	849	-1398	1026	-252	301	-556	-502	-679	-2718	864
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27	-700	-1461	227	1426	-299	-1272	551	-458	1442	-2234	-3021	-1283	1052	-2513	57	-408	29	-357	-2695	575
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-	-37	-10575	-5353	-732	-1329	-1781	-496	*	*											
28	-892	-1551	829	-1786	1667	-478	2447	-862	172	-702	-3207	181	657	-1619	734	-310	-335	-881	-1249	-1818
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-	-88	-10681	-4088	-732	-1329	-2756	-231	*	*											
29	-1497	55	-917	780	882	-954	1004	-1257	499	596	-3161	-2649	-966	-687	1631	-505	-72	-949	-457	523
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	-201	-10723	-2950	-732	-1329	-1997	-416	*	*											
33	451	-1007	-985	302	-774	-946	117	235	205	-2593	-3139	-2627	371	-2536	1181	627	1074	130	-2718	494
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34	-1996	68	-377	-969	-830	-188	1427	791	-25	-2742	102	-2776	120	996	-321	76	1047	1202	-2867	-572
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35	-698	-1667	-2825	-1534	-2683	-2275	482	52	-104	-2777	918	-2811	1688	-2720	601	1428	1104	-249	-2901	1130
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-	-1	-10700	-11700	-732	-1329	-2054	-398	*	*											
38	-554	-1629	-352	130	-758	-1248	-139	-982	774	-83	-251	-85	-76	-2681	793	-826	1955	-423	-2863	-577
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-	-1	-10773	-11773	-732	-1329	-1861	-465	*	*											
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-	-85	-10839	-4147	-732	-1329	-2049	-399	*	*											
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